

**Davis, Minh-Tam**

---

**To:** Schulwitz, Paul  
**Subject:** search for 09/700700

Thanks for your search result of SEQ ID NO:434 of 09/439313

However it seems that the search was not done against the parent cases of 09/439313, as requested, but rather against commercial data base, PGPUB and issued patents.

Could you please contact me ASAP because it is due this biweek.

Thanks.

MINH TAM DAVIS

305-2008

**THIS PAGE BLANK (USPTO)**



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 103561

**TO: Minh-Tam Davis**  
**Location: CM1/8A01&8E12**  
**Art Unit: 1642**  
**Saturday, September 13, 2003**  
**Case Serial Number: 09/700700**

**From: Paul Schulwitz**  
**Location: Biotech-Chem Library**  
**CM1-6B06**  
**Phone: 305-1954**

**paul.schulwitz@uspto.gov**

### Search Notes

Examiner Davis,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz  
Technical Information Specialist  
STIC Biotech/Chem Library  
(703)305-1954



**THIS PAGE BLANK (USPTO)**

103561

From: Hutzell, Paula  
Sent: Wednesday, September 10, 2003 1:57 PM  
To: STIC-Biotech/ChemLib; Davis, Minh-Tam  
Subject: FW: Rush search request for 09/700700

approved

-----Original Message-----

From: Davis, Minh-Tam  
Sent: Wednesday, September 10, 2003 9:04 AM  
To: Hutzell, Paula  
Subject: FW: Rush search request for 09/700700

Could you approve the rush request since Christina is out of the office today?  
ThanksTam

-----Original Message-----

Fr m: Davis, Minh-Tam  
Sent: Wednesday, September 10, 2003 9:02 AM  
To: Chan, Christina  
Subject: Rush search request for 09/700700

Please search SEQ ID NO:434 in the following parent cases of 09/439313 for priority date determination.

09439313 <snquery.pl?APPL\_ID=09439313>

**is a continuation in part of** 09352616 <snquery.pl?APPL\_ID=09352616>

**Which is a continuation in part of** 09288946 <snquery.pl?APPL\_ID=09288946>

**Which is a continuation in part of** 09232149 <snquery.pl?APPL\_ID=09232149>

**Which is a continuation in part of** 09159812 <snquery.pl?APPL\_ID=09159812>

**Which is a continuation in part of** 09115453 <snquery.pl?APPL\_ID=09115453>

**Which is a continuation in part of** 09030607 <snquery.pl?APPL\_ID=09030607>

**Which is a continuation in part of** 09020956 <snquery.pl?APPL\_ID=09020956>

**Which is a continuation in part of** 08904804 <snquery.pl?APPL\_ID=08904804>

**Which is a continuation in part of** 08806099 <snquery.pl?APPL\_ID=08806099>

Thank you.

MINH TAM DAVIS

ART UNIT 1642, ROOM 8A01, MB 8E12

305-2008

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 9/12  
Date Completed: 9/13  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OW nucleic - nucleic search, using sw model

Run on: September 13, 2003, 01:49:31 ; Search time 2165 seconds  
(without alignments)  
9145.616 Million cell updates/sec

Title: US-09-352-616A-434

Perfect score: 484

Sequence: 1 tttaaataagcatttagt.....ataaagtaccattgttttta 484

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rod.\*
- 36: em\_htg\_mam.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	484	100.0	484	6	AR261002 Sequence
2	484	100.0	484	6	AR278533 Sequence
3	484	100.0	484	6	AX106653 Sequence
4	484	100.0	484	6	AX140944 Sequence
5	484	100.0	484	6	AX200804 Sequence
6	484	100.0	484	6	AX267460 Sequence
7	472	97.5	2051	6	AR244306 Sequence
8	472	97.5	2984	6	AR237420 Sequence
9	472	97.5	2984	6	AR260913 Sequence
10	472	97.5	2984	6	AR278444 Sequence
11	472	97.5	2984	6	AX106211 Sequence
12	472	97.5	2984	6	AX106554 Sequence
13	472	97.5	2984	6	AX140845 Sequence
14	472	97.5	2984	6	AX200705 Sequence
15	472	97.5	2984	6	AX267361 Sequence
16	471	97.3	80586	9	AC012574 Homo sapi
17	471	97.3	174445	9	AC051642 Homo sapi
18	471	97.3	184361	2	AC022597 Homo sapi
19	455.4	94.1	3266	9	AF247704 Homo sapi
20	436.2	88.1	1020	6	AR244074 Sequence
21	426.2	88.1	1021	6	AR244075 Sequence
22	415.6	85.9	822	6	AR244195 Sequence
23	382.8	79.1	497	6	AR244194 Sequence
24	365	75.4	366	6	AR237207 Sequence
25	365	75.4	366	6	AR260700 Sequence
26	365	75.4	366	6	AR278231 Sequence
27	365	75.4	366	6	AX106334 Sequence
28	365	75.4	366	6	AX140625 Sequence
29	365	75.4	366	6	AX200485 Sequence
30	365	75.4	366	6	AX267141 Sequence
31	365	75.4	366	6	BD070260 Compounds
32	360	74.4	374	6	AX337002 Sequence
33	360	74.4	374	11	G37241 SHGC-57295
34	332	68.6	335	6	AR237233 Sequence
35	332	68.6	335	6	AR260726 Sequence
36	332	68.6	335	6	AR278257 Sequence
37	332	68.6	335	6	AX106360 Sequence
38	332	68.6	335	6	AX140651 Sequence
39	332	68.6	335	6	AX200511 Sequence
40	332	68.6	335	6	AX267167 Sequence
41	332	68.6	335	6	BD070286 Compounds
42	305.6	63.1	317	6	AR261021 Sequence
43	305.6	63.1	317	6	AR278552 Sequence
44	305.6	63.1	317	6	AX106672 Sequence
45	305.6	63.1	317	6	AX140963 Sequence

ALIGNMENTS

RESULT 1	AR261002	Sequence 434	484 bp	DNA	linear	PAT 29-JAN-2003
AR261002	LOCUS	Sequence 434	from patent US 6321716.			
DEFINITION	AR261002					
ACCESSION	AR261002					
VERSION	AR261002.1	GI:28071765				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 484)					
AUTHORS	Mashiki, Z. and Harada, J.					
TITLE	Negative pressure control apparatus for engine mounted in vehicle					
JOURNAL	Patent: US 6321716-A 434 27-NOV-2001;					
FEATURES	Location/Qualifiers					

5



```
Db 61 AATTAAATCTTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATATATTG 120
QY 121 TGTGCAAAAAAAGAGTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTTGC 180
Db 121 TGTGCAAAAAAAGAGTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTTGC 180
QY 181 TTTTCCCATTTGGAAGTCTGATTAACCCATCTCTGAACTGTGAGAAAAACATCTGAAG 240
Db 181 TTTTCCCATTTGGAAGTCTGATTAACCCATCTCTGAACTGTGAGAAAAACATCTGAAG 240
QY 241 AGCTAGTCTATCAGCATCTGACAGTCAATTTGCAAGGTTCTCAGAACCATTTCAACCAGA 300
Db 241 AGCTAGTCTATCAGCATCTGACAGTCAATTTGCAAGGTTCTCAGAACCATTTCAACCAGA 300
QY 301 CAGCCTGTTTCTATCTCTGTTTAAATTTAGTTTGGTTTCTCTACATGCATAACAAACC 360
Db 301 CAGCCTGTTTCTATCTCTGTTTAAATTTAGTTTGGTTTCTCTACATGCATAACAAACC 360
QY 361 TGTCTCAATCTGCACATAAAAGTCTGTGACTTGAAGTTTGTAGTCAGCACCCCAACAAAC 420
Db 361 TGTCTCAATCTGCACATAAAAGTCTGTGACTTGAAGTTTGTAGTCAGCACCCCAACAAAC 420
QY 421 TTTTATTTTCTATGTGTTTTCGCAACATATGAGTGTGTTTGAATAAAGTACCCATGTC 480
Db 421 TTTTATTTTCTATGTGTTTTCGCAACATATGAGTGTGTTTGAATAAAGTACCCATGTC 480
QY 481 TTTA 484
Db 481 TTTA 484

RESULT 4
AX200804
LOCUS AX140944 484 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 434 from Patent WO0134802.
ACCESSION AX140944
VERSION AX140944.1 GI:14281041
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Reed, S.G., Kalos, M.D., Retter, M.W., Stolk, J.A., Day, C.H.,
Skeiky, Y.A., and Wang, A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0134802-A 434 17-MAY-2001;
CORIXA CORPORATION (US)
FEATURES
source
1. .484
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 137 a 101 c 73 g 173 t
ORIGIN
Query Match 100.0%; Score 484; DB 6; Length 484;
Best Local Similarity 100.0%; Pred. No. 4.5e-105;
Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTAAATTAAGCATTTAGTGCCTCAGTCCCTACTGAGTACTCTTCTCCCTCCCTCTG 60
Db 1 TTTTAAATTAAGCATTTAGTGCCTCAGTCCCTACTGAGTACTCTTCTCCCTCCCTCTG 60
QY 61 AATTTAATTTCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATATATTG 120
Db 61 AATTTAATTTCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATATATTG 120
QY 121 TGTGCAAAAAAAGAGTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTTGC 180
Db 121 TGTGCAAAAAAAGAGTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTTGC 180
QY 181 TTTTCCCATTTGGAAGTCTGATTAACCCATCTCTGAACTGTGAGAAAAACATCTGAAG 240
Db 181 TTTTCCCATTTGGAAGTCTGATTAACCCATCTCTGAACTGTGAGAAAAACATCTGAAG 240
```

```
QY 181 TTTTCCCATTTGGAAGTCTGATTAACCCATCTCTGAACTGTGAGAAAAACATCTGAAG 240
Db 181 TTTTCCCATTTGGAAGTCTGATTAACCCATCTCTGAACTGTGAGAAAAACATCTGAAG 240
QY 241 AGCTAGTCTATCAGCATCTGACAGTCAATTTGCAAGGTTCTCAGAACCATTTCAACCAGA 300
Db 241 AGCTAGTCTATCAGCATCTGACAGTCAATTTGCAAGGTTCTCAGAACCATTTCAACCAGA 300
QY 301 CAGCCTGTTTCTATCTCTGTTTAAATTTAGTTTGGTTTCTCTACATGCATAACAAACC 360
Db 301 CAGCCTGTTTCTATCTCTGTTTAAATTTAGTTTGGTTTCTCTACATGCATAACAAACC 360
QY 361 TGTCTCAATCTGCACATAAAAGTCTGTGACTTGAAGTTTGTAGTCAGCACCCCAACAAAC 420
Db 361 TGTCTCAATCTGCACATAAAAGTCTGTGACTTGAAGTTTGTAGTCAGCACCCCAACAAAC 420
QY 421 TTTTATTTTCTATGTGTTTTCGCAACATATGAGTGTGTTTGAATAAAGTACCCATGTC 480
Db 421 TTTTATTTTCTATGTGTTTTCGCAACATATGAGTGTGTTTGAATAAAGTACCCATGTC 480
QY 481 TTTA 484
Db 481 TTTA 484

RESULT 5
AX200804
LOCUS AX200804 484 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 434 from Patent WO0151633.
ACCESSION AX200804
VERSION AX200804.1 GI:15390701
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Reed, S.G., Kalos, M.D., Fanger, G.R., Day, C.H., Retter, M.W.,
Stolk, J.A., Skeiky, Y.A., Wang, A., and Meagher, M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 434 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
source
1. .484
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 137 a 101 c 73 g 173 t
ORIGIN
Query Match 100.0%; Score 484; DB 6; Length 484;
Best Local Similarity 100.0%; Pred. No. 4.5e-105;
Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTAAATTAAGCATTTAGTGCCTCAGTCCCTACTGAGTACTCTTCTCCCTCCCTCTG 60
Db 1 TTTTAAATTAAGCATTTAGTGCCTCAGTCCCTACTGAGTACTCTTCTCCCTCCCTCTG 60
QY 61 AATTTAATTTCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATATATTG 120
Db 61 AATTTAATTTCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATATATTG 120
QY 121 TGTGCAAAAAAAGAGTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTTGC 180
Db 121 TGTGCAAAAAAAGAGTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTTGC 180
QY 181 TTTTCCCATTTGGAAGTCTGATTAACCCATCTCTGAACTGTGAGAAAAACATCTGAAG 240
Db 181 TTTTCCCATTTGGAAGTCTGATTAACCCATCTCTGAACTGTGAGAAAAACATCTGAAG 240
```

QY 241 AGCTAGTCTATCAGCATCTGACAGTGAATGGATGTTCTCAGAACCATTTACCCAGA 300  
|||||  
Db 241 AGCTAGTCTATCAGCATCTGACAGTGAATGGATGTTCTCAGAACCATTTACCCAGA 300  
QY 301 CAGCCTGTTCTATCCTCTTAAATAAATTAGTTTGGGTTCTCTACATGCAATAACACCC 360  
|||||  
Db 301 CAGCCTGTTCTATCCTCTTAAATAAATTAGTTTGGGTTCTCTACATGCAATAACACCC 360  
QY 361 TCGTCCAATCTGTCACATAAAAGTCTGTGACTTGAAGTTTAGTCAGCAGCCACCAAC 420  
|||||  
Db 361 TCGTCCAATCTGTCACATAAAAGTCTGTGACTTGAAGTTTAGTCAGCAGCCACCAAC 420  
QY 421 TTATTTTCTATGTTTGTGCAACATATGAGTGTGTTGAAATTAAGTACCCATGTC 480  
|||||  
Db 421 TTATTTTCTATGTTTGTGCAACATATGAGTGTGTTGAAATTAAGTACCCATGTC 480  
QY 481 TTTA 484  
|||||  
Db 481 TTTA 484  
RESULT 6  
AX267460  
LOCUS AX267460 484 bp DNA linear PAT 26-OCT-2001  
DEFINITION Sequence 434 from Patent WO0173032.  
ACCESSION AX267460  
VERSION AX267460.1 GI:16516224  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1  
Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,  
Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,  
Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A., Hepler, W.T.  
and Henderson, R.A.  
TITLE Compositions and methods for the therapy and diagnosis of prostate  
cancer  
JOURNAL Patent: WO 0173032-A 434 04-OCT-2001;  
CORIXA CORPORATION (US)  
FEATURES  
Source Location/Qualifiers  
1 .484  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 137 a 101 c 73 g 173 t  
ORIGIN  
Query Match 100.0%; Score 484; DB 6; Length 484;  
Best Local Similarity 100.0%; Pred. No. 4.5e-105;  
Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTAAATAAGCATTTAGTCTCAGTCCCTACTGAGTACTCTTCTCCCTCCCTCTG 60  
|||||  
Db 1 TTTTAAATAAGCATTTAGTCTCAGTCCCTACTGAGTACTCTTCTCCCTCCCTCTG 60  
QY 61 AATTAAATCTTCAACTGCAATTTGCAAGGATTACACATTTCACTGTGATGATATTG 120  
|||||  
Db 61 AATTAAATCTTCAACTGCAATTTGCAAGGATTACACATTTCACTGTGATGATATTG 120  
QY 121 TGTGCAAAAAAAGGTCTTTGTTTAAATTAATTTACTGTTTGAATCCATCTGC 180  
|||||  
Db 121 TGTGCAAAAAAAGGTCTTTGTTTAAATTAATTTACTGTTTGAATCCATCTGC 180  
QY 181 TTTTCCCAATGGAAGTCTGTTTAAATTAATTTACTGTTTGAATCCATCTGC 240  
|||||  
Db 181 TTTTCCCAATGGAAGTCTGTTTAAATTAATTTACTGTTTGAATCCATCTGC 240  
QY 241 AGCTAGTCTATCAGCATCTGACAGTGAATGGATGTTCTCAGAACCATTTACCCAGA 300  
|||||  
Db 241 AGCTAGTCTATCAGCATCTGACAGTGAATGGATGTTCTCAGAACCATTTACCCAGA 300

QY 301 CAGCCTGTTCTATCCTCTTAAATAAATTAGTTTGGGTTCTCTACATGCAATAACACCC 360  
|||||  
Db 301 CAGCCTGTTCTATCCTCTTAAATAAATTAGTTTGGGTTCTCTACATGCAATAACACCC 360  
QY 361 TCGTCCAATCTGTCACATAAAAGTCTGTGACTTGAAGTTTAGTCAGCAGCCACCAAC 420  
|||||  
Db 361 TCGTCCAATCTGTCACATAAAAGTCTGTGACTTGAAGTTTAGTCAGCAGCCACCAAC 420  
QY 421 TTATTTTCTATGTTTGTGCAACATATGAGTGTGTTGAAATTAAGTACCCATGTC 480  
|||||  
Db 421 TTATTTTCTATGTTTGTGCAACATATGAGTGTGTTGAAATTAAGTACCCATGTC 480  
QY 481 TTTA 484  
|||||  
Db 481 TTTA 484  
RESULT 7  
AR244306/c  
LOCUS AR244306 2051 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 334 from patent US 6476207.  
ACCESSION AR244306  
VERSION AR244306.1 GI:27292093  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 2051)  
AUTHORS Zhang, J., Astle, J.H., Carroll, E. III, Endege, W.O., Ford, D.M.,  
Monahan, J.E., Schlegel, R. and Steinmann, K.E.  
TITLE Genes and gene expression products that are differentially  
regulated in prostate cancer  
JOURNAL Patent: US 6476207-A 334 05-NOV-2002;  
FEATURES Location/Qualifiers  
1 .2051  
/organism="unknown"  
BASE COUNT 630 a 427 c 408 g 555 t 31 others  
ORIGIN  
Query Match 97.5%; Score 472; DB 6; Length 2051;  
Best Local Similarity 99.6%; Pred. No. 2.8e-102;  
Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;  
QY 1 TTTTAAATAAGCATTTAGTCTCAGTCCCTACTGAGTACTCTTCTCCCTCCCTCTG 60  
Db 854 TTTTAAATAAGCATTTAGTCTCAGTCCCTACTGAGTACTCTTCTCCCTCCCTCTG 795  
QY 61 AATTAAATCTTCAACTTGAATTTGCAAGGATTACACATTTCACTGTGATGATATTG 120  
Db 794 AATTAAATCTTCAACTTGAATTTGCAAGGATTACACATTTCACTGTGATGATATTG 735  
QY 121 TGTTCG--AAAAAAGTGTCTTGTGTTAAATTAATTTACTTGGTTTGTGAATCCATCT 178  
Db 734 TGTGCAAAAAAAGGTGTCTTGTGTTAAATTAATTTACTTGGTTTGTGAATCCATCT 675  
QY 179 GCTTTTCCCAATGGAAGTCTGTTTAAATTAATTTACTTGGTTTGTGAATCCATCT 238  
Db 674 GCTTTTCCCAATGGAAGTCTGTTTAAATTAATTTACTTGGTTTGTGAATCCATCT 615  
QY 239 AGAGTAGTCTATCAGCATCTGACAGTGAATTCGATGTTCTCAGAACCATTTTCCACCA 298  
Db 614 AGAGTAGTCTATCAGCATCTGACAGTGAATTCGATGTTCTCAGAACCATTTTCCACCA 555  
QY 299 GACAGCCTGTTCTATCCTCTTAAATTAATTTAGTGTGTTGTTCTCATGTCATAACAA 358  
Db 554 GACAGCCTGTTCTATCCTCTTAAATTAATTTAGTGTGTTGTTCTCATGTCATAACAA 495  
QY 359 CCTGCTCCAATCTGTCACATAAAAGTCTGTGACTTGAAGTTTAGTCAGCAGCCACCA 418  
Db 494 CCTGCTCCAATCTGTCACATAAAAGTCTGTGACTTGAAGTTTAGTCAGCAGCCACCA 435  
QY 419 ACTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTGAAATTAAGTACCCATG 478  
|||||



JOURNAL  
FEATURES  
source  
Patent: US 6512094-A 335 28-JAN-2003;  
Location/Qualifiers  
1. .2984  
/organism="unknown"

BASE COUNT 837 a 659 c 645 g 842 t 1 others  
ORIGIN

Query Match 97.5%; Score 472; DB 6; Length 2984;  
Best Local Similarity 99.6%; Pred. No. 2.7e-102;  
Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;  
1 TTTTAAATAAGCATTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCCTCTG 60  
2473 TTTTAAATAAGCATTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCCTCTG 2532  
61 AATTAAATCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATATATTG 120  
2533 AATTAAATCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATATATTG 2592  
121 TGTTCG--AAAAAAGAGTCTTTGTTTAAATTTACTTGGTTTGAATCCATCTT 178  
2593 TGTTCGAAAAAAGAGTCTTTGTTTAAATTTACTTGGTTTGAATCCATCTT 2652  
179 GCTTTTCCCATTTGGAAGTCTTAAATTTACTTGGTTTGAATCCATCTT 238  
2653 GCTTTTCCCATTTGGAAGTCTTAAATTTACTTGGTTTGAATCCATCTT 2712  
239 AGAGCTAGTCTATCAGCATCTGACAGTGAATTTGGATGTTCTCAGAACCATCTCGA 298  
2713 AGAGCTAGTCTATCAGCATCTGACAGTGAATTTGGATGTTCTCAGAACCATCTCGA 2772  
299 GACAGCCTGTTCTATCCTCTGTTTAAATTTACTTGGTTTGAATCCATCTT 358  
2773 GACAGCCTGTTCTATCCTCTGTTTAAATTTACTTGGTTTGAATCCATCTT 2832  
359 CTTGCTCCATCTGTCACATAAAGTCTGTGACTTGAAGTTAGTCAGCAGCCACCA 418  
2833 CTTGCTCCATCTGTCACATAAAGTCTGTGACTTGAAGTTAGTCAGCAGCCACCA 2892  
419 ACTTAAATTTCTATGTTTGAATTTAGTCAGCAGCCACCA 478  
2893 ACTTAAATTTCTATGTTTGAATTTAGTCAGCAGCCACCA 2952  
479 TCTTTA 484  
2953 TCTTTA 2958

RESULT 11  
AX106211  
LOCUS  
DEFINITION  
Sequence 349 from Patent WO0125273.  
AX106211  
VERSION  
AX106211.1 GI:13921900  
KEYWORDS  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
Skeiky, Y.A., Xu, J., Cheever, M.A. and Reed, S.G.  
Compositions and methods for wt1 specific immunotherapy  
Patent: WO 0125273-A 349 12-APR-2001;  
CORIXA CORPORATION (US)  
FEATURES  
source  
Location/Qualifiers  
1. .2984  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 837 a 659 c 645 g 842 t 1 others  
ORIGIN

Query Match 97.5%; Score 472; DB 6; Length 2984;  
Best Local Similarity 99.6%; Pred. No. 2.7e-102;  
Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;  
1 TTTTAAATAAGCATTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCCTCTG 60  
2473 TTTTAAATAAGCATTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCCTCTG 2532  
61 AATTAAATCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATATATTG 120  
2533 AATTAAATCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATATATTG 2592  
121 TGTTCG--AAAAAAGAGTCTTTGTTTAAATTTACTTGGTTTGAATCCATCTT 178  
2593 TGTTCGAAAAAAGAGTCTTTGTTTAAATTTACTTGGTTTGAATCCATCTT 2652  
179 GCTTTTCCCATTTGGAAGTCTTAAATTTACTTGGTTTGAATCCATCTT 238  
2653 GCTTTTCCCATTTGGAAGTCTTAAATTTACTTGGTTTGAATCCATCTT 2712  
239 AGAGCTAGTCTATCAGCATCTGACAGTGAATTTGGATGTTCTCAGAACCATCTCGA 298  
2713 AGAGCTAGTCTATCAGCATCTGACAGTGAATTTGGATGTTCTCAGAACCATCTCGA 2772  
299 GACAGCCTGTTCTATCCTCTGTTTAAATTTACTTGGTTTGAATCCATCTT 358  
2773 GACAGCCTGTTCTATCCTCTGTTTAAATTTACTTGGTTTGAATCCATCTT 2832  
359 CTTGCTCCATCTGTCACATAAAGTCTGTGACTTGAAGTTAGTCAGCAGCCACCA 418  
2833 CTTGCTCCATCTGTCACATAAAGTCTGTGACTTGAAGTTAGTCAGCAGCCACCA 2892  
419 ACTTAAATTTCTATGTTTGAATTTAGTCAGCAGCCACCA 478  
2893 ACTTAAATTTCTATGTTTGAATTTAGTCAGCAGCCACCA 2952  
479 TCTTTA 484  
2953 TCTTTA 2958

RESULT 12  
AX106554  
LOCUS  
DEFINITION  
Sequence 335 from Patent WO0125272.  
AX106554  
VERSION  
AX106554.1 GI:13922229  
KEYWORDS  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
Xu, J., Skeiky, Y.A., Reed, S.G. and Cheever, M.A.  
Compositions and methods for therapy and diagnosis of prostate  
cancer.  
Patent: WO 0125272-A 335 12-APR-2001;  
CORIXA CORPORATION (US)  
FEATURES  
source  
Location/Qualifiers  
1. .2984  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 837 a 659 c 645 g 842 t 1 others  
ORIGIN

Query Match 97.5%; Score 472; DB 6; Length 2984;  
Best Local Similarity 99.6%; Pred. No. 2.7e-102;  
Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;  
1 TTTTAAATAAGCATTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCCTCTG 60  
2473 TTTTAAATAAGCATTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCCTCTG 2532

```
Qy 61 AATTAATCTTTCAACTTGCATTTTGAAGGATTACACATTTTCACTGTGATGATATG 120
D 2533 AATTAATCTTTCAACTTGCATTTTGAAGGATTACACATTTTCACTGTGATGATATG 2592
Qy 121 TGTTCG--AAAAAAGAGTGTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTT 178
D 2593 TGTTCGAAAAAAGAGTGTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTT 2652
Qy 179 GCTTTTCCCATTTGGAAGTGTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTT 238
D 2653 GCTTTTCCCATTTGGAAGTGTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTT 2712
Qy 239 AGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGATGGTTTCTCAGAACCATTTTCAACCA 298
D 2713 AGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGATGGTTTCTCAGAACCATTTTCAACCA 2772
Qy 299 GACAGCTGTTTCTATCCTGTTTAAATTTAGTTTGGTTTCTCAGAACCATTTTCAACCA 358
D 2773 GACAGCTGTTTCTATCCTGTTTAAATTTAGTTTGGTTTCTCAGAACCATTTTCAACCA 2832
Qy 359 CCTGCTCCATCTGTCACATAAAGTCTGTGACTTGAAGTTTGTGAAAAATAAGTACCCTATG 418
D 2833 CCTGCTCCATCTGTCACATAAAGTCTGTGACTTGAAGTTTGTGAAAAATAAGTACCCTATG 2892
Qy 419 ACTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATAATAAGTACCCTATG 478
D 2893 ACTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATAATAAGTACCCTATG 2952
Qy 479 TCCTTA 484
D 2953 TCCTTA 2958
```

```
RESULT 13
AX140845
LOCUS AX140845 2984 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 335 from Patent WO0134802.
ACCESSION AX140845
VERSION AX140845.1 GI:14280952
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Retter,M.W., Stoik,J.A., Day,C.H.,
Skeiky,Y.A. and Wang,A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0134802-A 335 17-MAY-2001;
CORIXA CORPORATION (US)
FEATURES
source
1. .2984
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 837 a 659 c 645 g 842 t 1 others
ORIGIN
Query Match 97.5%; Score 472; DB 6; Length 2984;
Best Local Similarity 99.6%; Pred. No. 2.7e-102;
Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
```

```
Qy 1 TTTTAAATAGCATTTAGTGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCCTCTG 60
D 2473 TTTTAAATAGCATTTAGTGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCCTCTG 2532
Qy 61 AATTAATCTTTCAACTTGCATTTTGAAGGATTACACATTTTCACTGTGATGATATG 120
D 2533 AATTAATCTTTCAACTTGCATTTTGAAGGATTACACATTTTCACTGTGATGATATG 2592
```

```
Qy 121 TGTTCG--AAAAAAGAGTGTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTT 178
D 2593 TGTTCGAAAAAAGAGTGTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTT 2652
Qy 179 GCTTTTCCCATTTGGAAGTGTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTG 238
D 2653 GCTTTTCCCATTTGGAAGTGTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTG 2712
Qy 239 AGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGATGGTTTCTCAGAACCATTTTCAACCA 298
D 2713 AGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGATGGTTTCTCAGAACCATTTTCAACCA 2772
Qy 299 GACAGCTGTTTCTATCCTGTTTAAATTTAGTTTGGTTTCTCAGAACCATTTTCAACCA 358
D 2773 GACAGCTGTTTCTATCCTGTTTAAATTTAGTTTGGTTTCTCAGAACCATTTTCAACCA 2832
Qy 359 CCTGCTCCATCTGTCACATAAAGTCTGTGACTTGAAGTTTGTGAAAAATAAGTACCCTATG 418
D 2833 CCTGCTCCATCTGTCACATAAAGTCTGTGACTTGAAGTTTGTGAAAAATAAGTACCCTATG 2892
Qy 419 ACTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATAATAAGTACCCTATG 478
D 2893 ACTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATAATAAGTACCCTATG 2952
Qy 479 TCCTTA 484
D 2953 TCCTTA 2958
```

```
RESULT 14
AX200705
LOCUS AX200705 2984 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 335 from Patent WO0151633.
ACCESSION AX200705
VERSION AX200705.1 GI:15390594
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stoik,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 335 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
source
1. .2984
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 837 a 659 c 645 g 842 t 1 others
ORIGIN
```

```
Query Match 97.5%; Score 472; DB 6; Length 2984;
Best Local Similarity 99.6%; Pred. No. 2.7e-102;
Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
Qy 1 TTTTAAATAGCATTTAGTGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCCTCTG 60
D 2473 TTTTAAATAGCATTTAGTGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCCTCTG 2532
Qy 61 AATTAATCTTTCAACTTGCATTTTGAAGGATTACACATTTTCACTGTGATGATATG 120
D 2533 AATTAATCTTTCAACTTGCATTTTGAAGGATTACACATTTTCACTGTGATGATATG 2592
Qy 121 TGTTCG--AAAAAAGAGTGTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTT 178
D 2593 TGTTCGAAAAAAGAGTGTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTT 2652
Qy 179 GCTTTTCCCATTTGGAAGTGTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTG 238
```

```

Db      2653 GCTTTTCCCATTTGGAACCTAGTCAATTAACCCATCTCTGAACTGGTAGAAAAACATCTGA 2712
QY      239 AGAGCTAGTCTATCAGCATCTCAGAGTGAAATTCGATGGTCTCAGAACCAATTTACCCCA 298
Db      2713 AGAGCTAGTCTATCAGCATCTCAGAGTGAAATTCGATGGTCTCAGAACCAATTTACCCCA 2772
QY      299 GACAGCCGTGTTCTATCCTGTTTAAATAAATAGTTTGGGTTCTACATGCATACAAAC 358
Db      2773 GACAGCCGTGTTCTATCCTGTTTAAATAAATAGTTTGGGTTCTACATGCATACAAAC 2832
QY      359 COTGCTCAATCTGTCACATAAAGTCTGACCTTGAAGTTAGTCAGCACCCCCACCAA 418
Db      2833 COTGCTCAATCTGTCACATAAAGTCTGACCTTGAAGTTAGTCAGCACCCCCACCAA 2892
QY      419 ACTTTATTTTCTATGTTTGTGGAACATATGAGTGTGTTGAAATAAAGTACCCCATG 478
Db      2893 ACTTTATTTTCTATGTTTGTGGAACATATGAGTGTGTTGAAATAAAGTACCCCATG 2952
QY      479 TCTTTA 484
Db      2953 TCTTTA 2958

```

## RESULT 15

```

AX267361
LOCUS      AX267361
DEFINITION Sequence 335 from Patent WO0173032.
ACCESSION AX267361
VERSION   AX267361.1 GI:16516135
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
REFERENCE
AUTHORS   Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
          Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
          Vedwick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
          and Henderson,R.A.
TITLE     Compositions and methods for the therapy and diagnosis of prostate
          cancer
JOURNAL   Patent: WO 0173032-A 335 04-OCT-2001;
          CORIXA CORPORATION (US)
FEATURES
source    1. .2984
          /organism="Homo sapiens"
          /mol_type="genomic DNA"
          /db_xref="taxon:9606"
BASE COUNT 837 a 659 c 645 g 842 t 1 others
ORIGIN

```

```

Query Match
Best Local Similarity 97.5%; Score 472; DB 6; Length 2984;
Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
QY      1 TTTTAAATAAGCATTTAGTGTCTCAGTCCCTACTGAGTACTCTTCTCTCCCTCTCTCTG 60
Db      2473 TTTTAAATAAGCATTTAGTGTCTCAGTCCCTACTGAGTACTCTTCTCTCCCTCTCTCTG 2532
QY      61 AATTTAATCTTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATGATATG 120
Db      2533 AATTTAATCTTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATGATATG 2592
QY      121 TGTGTC--AAAAAAGAGTGTCTTTGTTTAAATTTACTTTGGTTGGTGAATCCATCTT 178
Db      2593 TGTGTC--AAAAAAGAGTGTCTTTGTTTAAATTTACTTTGGTTGGTGAATCCATCTT 2652
QY      179 GCTTTTCCCATTTGGAACCTAGTCAATTAACCCATCTCTGAACTGGTAGAAAAACATCTGA 238
Db      2653 GCTTTTCCCATTTGGAACCTAGTCAATTAACCCATCTCTGAACTGGTAGAAAAACATCTGA 2712
QY      239 AGAGCTAGTCTATCAGCATCTCAGAGTGAAATTCGATGGTCTCTCAGAACCAATTTACCCCA 298

```

```

Db      2713 AGAGCTAGTCTATCAGCATCTCAGAGTGAAATTCGATGGTCTCTCAGAACCAATTTACCCCA 2772
QY      299 GACAGCCGTGTTTCTATCCTGTTTAAATAAATAGTTTGGGTTCTCTACATGCATACAAAC 358
Db      2773 GACAGCCGTGTTTCTATCCTGTTTAAATAAATAGTTTGGGTTCTCTACATGCATACAAAC 2832
QY      359 COTGCTCAATCTGTCACATAAAGTCTGACCTTGAAGTTAGTCAGCACCCCCACCAA 418
Db      2833 COTGCTCAATCTGTCACATAAAGTCTGACCTTGAAGTTAGTCAGCACCCCCACCAA 2892
QY      419 ACTTTATTTTCTATGTTTGTGGAACATATGAGTGTGTTGAAATAAAGTACCCCATG 478
Db      2893 ACTTTATTTTCTATGTTTGTGGAACATATGAGTGTGTTGAAATAAAGTACCCCATG 2952
QY      479 TCTTTA 484
Db      2953 TCTTTA 2958

```

Search completed: September 13, 2003, 03:04:39  
Job time : 2168 secs

GenCore version 5.1.6									
Copyright (c) 1993 - 2003 Compugen Ltd.									
OM nucleic - nucleic search, using sw model									
Run on:	September 12, 2003, 23:52:20 ; Search time 225 Seconds (without alignments) 5806.791 Million cell updates/sec								
Title:	US-09-352-616A-434								
Perfect score:	484								
Sequence:	1 ttttaataataagcattagt.....ataaagtaccatgctcttta 484								
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0								
Searched:	2552756 seqs, 1349719017 residues								
Total number of hits satisfying chosen parameters:	5105512								
Minimum DB seq length:	0								
Maximum DB seq length:	2000000000								
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries								
Database :	N_Geneseq_19Jun03.*								
1:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*								
2:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*								
3:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*								
4:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*								
5:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*								
6:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*								
7:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*								
8:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*								
9:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*								
10:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*								
11:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*								
12:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*								
13:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*								
14:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*								
15:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*								
16:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*								
17:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*								
18:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*								
19:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*								
20:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*								
21:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*								
22:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*								
23:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*								
24:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*								
25:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*								
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result No.	Score	Query Match	Length	DB ID	Description				
1	484	100.0	484	21	AAA06653	Human immunogenic			
2	484	100.0	484	22	AAAG3862	Human prostate cDN			
3	484	100.0	484	22	AAH93769	Human prostate-spe			
4	484	100.0	484	22	AAH85083	Human prostate-spe			
5	484	100.0	484	22	AAH02834	Prostate tumour an			
6	484	100.0	484	24	ABL95233	Human 22595 cDNA s			
7	484	100.0	484	25	ACA59670	Prostate cancer th			
8	473	97.7	755	21	AAFI5823	Human prostate can			

c	9	472	97.5	2051	21	AAZ97473	Human prostate can
	10	472	97.5	2984	21	AAA06564	Human immunogenic
	11	472	97.5	2984	22	AAAG3773	Human prostate cDN
	12	472	97.5	2984	22	AAH93680	Human prostate-spe
	13	472	97.5	2984	22	AAH84994	Human prostate-spe
	14	472	97.5	2984	22	AAH02745	Prostate tumour an
	15	472	97.5	2984	22	AAAF86953	Human p705P invent
	16	472	97.5	2984	24	ABL95144	Human p705P cDNA s
	17	472	97.5	2984	25	ACA59581	Prostate cancer th
	18	469.4	97.0	1936	21	AAZ45667	Nucleotide sequenc
	19	448	92.6	1191	23	ABV24315	Human prostate exp
	20	448	92.6	1191	23	ABV24721	Human prostate exp
	21	448	92.6	1191	23	ABV24938	Human prostate can
	22	426.2	88.1	1020	21	AAZ97241	Human prostate can
	23	426.2	88.1	1021	21	AAZ97242	Human prostate can
	24	415.6	85.9	822	21	AAZ97362	Human prostate can
	25	382.8	79.1	497	21	AAZ97361	Human prostate can
	26	365	75.4	366	19	AAV61203	cDNA sequence of p
	27	365	75.4	366	19	AAV58588	Prostate tumour sp
	28	365	75.4	366	21	AAA06351	Human immunogenic
	29	365	75.4	366	22	AAAG3559	Human prostate cDN
	30	365	75.4	366	22	AAAS10110	Human prostate tum
	31	365	75.4	366	22	AAH93467	Human prostate-spe
	32	365	75.4	366	22	AAH84781	Human prostate-spe
	33	365	75.4	366	22	AAH02532	Prostate tumour an
	34	365	75.4	366	24	ABS71256	Human prostate tum
	35	365	75.4	366	24	ABS58640	Prostate tumour CD
	36	365	75.4	366	24	ABL94931	Human p89 cDNA seq
	37	365	75.4	366	25	ACA59368	Prostate cancer th
	38	360	74.4	374	24	ABL69174	Prostate cancer re
	39	359	74.2	525	23	ABV24198	Human prostate exp
	40	332	68.6	335	19	AAV61229	cDNA sequence of p
	41	332	68.6	335	19	AAV58614	Prostate tumour sp
	42	332	68.6	335	21	AAA06377	Human immunogenic
	43	332	68.6	335	22	AAAG3585	Human prostate cDN
	44	332	68.6	335	22	AAAS10136	Human prostate tum
	45	332	68.6	335	22	AAH93493	Human prostate-spe

ALIGNMENTS

RESULT 1

AAA06653

ID AAA06653 standard; cDNA; 484 BP.

XX

AC AAA06653;

XX

DT 13-JUN-2000 (first entry)

XX

DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:434.

XX

KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;

XX

KW immunogenic; cytostatic; vaccine; ss.

XX

OS Homo sapiens.

XX

PN WO200004149-A2.

XX

PD 27-JAN-2000.

XX

PF 14-JUL-1999; 99WO-US15838.

XX

PR 14-JUL-1998; 98US-0115453.

XX

PR 14-JUL-1998; 98US-0116134.

XX

PR 23-SEP-1998; 98US-0159812.

XX

PR 23-SEP-1998; 98US-0159822.

XX

PR 15-JAN-1999; 99US-0232149.

XX

PR 15-JAN-1999; 99US-0232880.

XX

PR 09-APR-1999; 99US-0288946.

XX

PA (CORI-) CORIXA CORP.

XX

PI Dillon DC, Harlocker SL, Yuqiu J, Xu J, Mitcham JL;  
XX WPI; 2000-171268/15.  
DR  
XX  
XX  
PT New polypeptide useful for treating and diagnosing prostate cancer  
PT comprises an immunogenic portion of prostate tumor protein -  
XX  
XX  
PS Claim 1; Page 250; 263pp; English.  
XX  
CC The present invention describes isolated polypeptides, comprising an  
CC immunogenic portion of a prostate tumor protein (PIP). The polypeptides  
CC and polynucleotides encoding them have cytostatic activity and can be  
CC used in vaccines and in gene therapy. The polypeptides and  
CC polynucleotides encoding them, antigen presenting cells which express  
CC the polypeptides, antibodies against the polypeptides and vaccines  
CC comprising them can be used for inhibiting the development of prostate  
CC cancer in a patient. The polypeptides can be used to generate antibodies  
CC or anti-idiotypic antibodies for passive immuno therapy. A portion of  
CC the polynucleotides encoding the polypeptides can be used as a probe or  
CC to modulate the expression of the polypeptides. AA06241 to AA06691 and  
CC AY82000 to AY82020 represent sequences used in the exemplification of  
CC the present invention.  
XX  
SQ Sequence 484 BP; 137 A; 101 C; 73 G; 173 T; 0 other;  
Query Match 100.0%; Score 484; DB 21; Length 484;  
Best Local Similarity 100.0%; Pred. No. 1.4e-116; Indels 0; Gaps 0;  
Matches 484; Conservative 0; Mismatches 0;  
QY 1 TTTTAAATAAGCAATTAGTCTAGTCCCTACTGAGTACTCTTTCTCTCCCTCTCTG 60  
DB 1 TTTTAAATAAGCAATTAGTCTAGTCCCTACTGAGTACTCTTTCTCTCCCTCTCTG 60  
QY 61 AATTAAATCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATATATG 120  
DB 61 AATTAAATCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATATATG 120  
QY 121 TGTGCAAAAAAAGAGTCTTTGTTTAAATTAATCTTGTGATATATATG 180  
DB 121 TGTGCAAAAAAAGAGTCTTTGTTTAAATTAATCTTGTGATATATATG 180  
QY 181 TTTTCCCATTTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 240  
DB 181 TTTTCCCATTTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 240  
QY 241 AGCTAGTCTATGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 300  
DB 241 AGCTAGTCTATGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 300  
QY 301 CAGCCTGTTTCTATCTGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 360  
DB 301 CAGCCTGTTTCTATCTGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 360  
QY 361 TGCTCAATCTGTACATAAAAGTCTGTCACTTGAAGTTTGTGAGTCTGAGTCTGAGTCTGAG 420  
DB 361 TGCTCAATCTGTACATAAAAGTCTGTCACTTGAAGTTTGTGAGTCTGAGTCTGAGTCTGAG 420  
QY 421 TTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATTAATTAATTAATTAATTAAT 480  
DB 421 TTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATTAATTAATTAATTAATTAAT 480  
QY 481 TTTA 484  
DB 481 TTTA 484  
RESULT 2  
AAS63862  
ID AAS63862 standard; cDNA; 484 BP.  
XX  
AC AAS63862;  
XX  
DT 29-JAN-2002 (first entry)

XX Human prostate cDNA sequence #398.  
DE  
XX  
XX  
KW Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.  
XX  
OS Homo sapiens.  
XX  
PN WO200173032-A2.  
XX  
PD 04-OCT-2001.  
XX  
PF 27-MAR-2001; 2001WO-0509919.  
XX  
PR 27-MAR-2000; 2000US-0536857.  
PR 09-MAY-2000; 2000US-0568100.  
PR 12-MAY-2000; 2000US-0570737.  
PR 13-JUN-2000; 2000US-0593793.  
PR 27-JUN-2000; 2000US-0605783.  
PR 10-AUG-2000; 2000US-0636215.  
PR 29-AUG-2000; 2000US-0651236.  
PR 06-SEP-2000; 2000US-0657279.  
PR 02-OCT-2000; 2000US-0679426.  
PR 10-OCT-2000; 2000US-0685166.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;  
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;  
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;  
XX WPI; 2001-639232/73.  
DR  
XX  
XX New human prostate-specific polypeptides and polynucleotides useful for  
PT the diagnosis and treatment of cancer, especially prostate cancer -  
PT  
XX  
PS Claim 1; Page 375; 579pp; English.  
XX  
CC The invention relates to isolated prostate-specific  
CC polynucleotides, polypeptides, fusion proteins of the polypeptides,  
CC antibodies raised against the polypeptides (or antigenic epitopes,  
CC derived from them) and antigen-presenting cells expressing the  
CC polypeptides. The antibodies are useful for detecting the presence of  
CC cancer, especially prostate cancer. The polypeptides, polynucleotides and  
CC the antigen-presenting cells are useful for stimulating the presence of  
CC t cells specific for a tumour protein, and for inhibiting the development  
CC of cancer especially prostate cancer. Compositions comprising an immune  
CC polynucleotide and/or polypeptide are useful for stimulating an immune  
CC response, and for treating cancer. The oligonucleotide is useful for  
CC detecting cancer. The present sequence is a prostate specific  
CC polynucleotide of the invention.  
XX  
SQ Sequence 484 BP; 137 A; 101 C; 73 G; 173 T; 0 other;  
Query Match 100.0%; Score 484; DB 22; Length 484;  
Best Local Similarity 100.0%; Pred. No. 1.4e-116;  
Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTAAATAAGCAATTAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 60  
DB 1 TTTTAAATAAGCAATTAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 60  
QY 61 AATTAAATCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATATATG 120  
DB 61 AATTAAATCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATATATG 120  
QY 121 TGTGCAAAAAAAGAGTCTTTGTTTAAATTAATCTTGTGATATATATG 180  
DB 121 TGTGCAAAAAAAGAGTCTTTGTTTAAATTAATCTTGTGATATATATG 180  
QY 181 TTTTCCCATTTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 240  
DB 181 TTTTCCCATTTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 240



QY 241 AGCTAGTCTATCAGCATCTGACAGTGTAATGGATGGTTCTCAGAACCATTTTACCACGAGA 300  
Db |||||||  
QY 241 AGCTAGTCTATCAGCATCTGACAGTGTAATGGATGGTTCTCAGAACCATTTTACCACGAGA 300  
Db |||||||  
QY 301 CAGCCTGTTCTATCCTGTTTAAATAAATTAGTTTGGGTTCTCAGCATGATTAACAACCC 360  
Db |||||||  
QY 301 CAGCCTGTTCTATCCTGTTTAAATAAATTAGTTTGGGTTCTCAGCATGATTAACAACCC 360  
Db |||||||  
QY 361 TGCTCCCAATCTGTCACATAAAAGTCTGTGACTTTGAAGTTTGTAGTCAGCACCCCCACCACAAAC 420  
Db TGCTCCCAATCTGTCACATAAAAGTCTGTGACTTTGAAGTTTGTAGTCAGCACCCCCACCACAAAC 420  
QY 421 TTTATTTTTCATGTGTTTGGCAACATATGAGTGTGTTTGAATAAAGTACCACATGTC 480  
Db TTTATTTTTCATGTGTTTGGCAACATATGAGTGTGTTTGAATAAAGTACCACATGTC 480  
QY 481 TTTA 484  
Db |||||  
QY 481 TTTA 484

RESULT 3

AAH93769  
ID AAH93769 standard; cDNA; 484 BP.  
XX  
AC AAH93769;  
XX  
DT 04-OCT-2001 (first entry)  
XX  
DE Human prostate-specific cDNA sequence 22595.  
XX  
KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;  
KW cytostatic; gene therapy; metastasis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200151633-A2.  
XX  
PD 19-JUL-2001.  
XX  
PF 16-JAN-2001; 2001WO-US01574.  
XX  
PR 14-JAN-2000; 2000US-0483672.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;  
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skelky YAW;  
PI Wang A, Meagher MJ;  
XX  
DR WPI; 2001-425873/45.  
XX  
PS New polynucleotide encoding a prostate-specific protein, for  
PT diagnosing, monitoring and treating prostate cancer in a patient and  
PT for use in vaccines -  
XX  
PS Claim 1; Page 373; 543pp; English.  
XX  
CC The present invention describes polynucleotide sequences (I) which encode  
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,  
CC and can be used in vaccine production and gene therapy. (I), (II),  
CC antibodies to (II), fusion proteins comprising (II), and isolated  
CC T cells prepared using (I) or (II) are used treat cancer in a patient.  
CC (I) and the antibodies are also used in the detection of cancer in a  
CC patient. The cancer that is diagnosed or treated is particularly  
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or  
CC (I) can be used for monitoring the progression of cancer in a patient.  
CC (I) and (II) can also be used to improve diagnostic and therapeutic  
CC methods for prostate cancer. They can indicate the level of metastasis  
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to  
CC AAH01318 represent polynucleotide and amino acid sequences used in the  
CC exemplification of the present invention.  
XX

SQ Sequence 484 BP; 137 A; 101 C; 73 G; 173 T; 0 other;  
Query Match 100.0%; Score 484; DB 22; Length 484;  
Best Local Similarity 100.0%; Pred. No. 1.4e-116;  
Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTAAATAAGCATTTTAGTCTCAGTCCCTACTGAGTACTCTTCTCTCCCTCCCTCTG 60  
Db 1 TTTTAAATAAGCATTTTAGTCTCAGTCCCTACTGAGTACTCTTCTCTCCCTCCCTCTG 60  
QY 61 AATTTAAATCTCTTCAACTTGCAGATTTGCAAGGATTACACATTTTCACTGTGATGATATTG 120  
Db 61 AATTTAAATCTCTTCAACTTGCAGATTTGCAAGGATTACACATTTTCACTGTGATGATATTG 120  
QY 121 TGTTCGAAAAAAGAGTGTCTTGTGTTTAAAAATTACTTGGTTTGTGAATCCATCTTGC 180  
Db 121 TGTTCGAAAAAAGAGTGTCTTGTGTTTAAAAATTACTTGGTTTGTGAATCCATCTTGC 180  
QY 181 TTTTTCGCCATTTGGAACCTAGTCATTAACCCATCTCTGAACCTGGTAGAAAAACATCTGAAG 240  
Db 181 TTTTTCGCCATTTGGAACCTAGTCATTAACCCATCTCTGAACCTGGTAGAAAAACATCTGAAG 240  
QY 241 AGCTAGTCTATCAGCATCTGACAGTGTAATGGATGGTTCTCAGAACCATTTTACCACGAGA 300  
Db 241 AGCTAGTCTATCAGCATCTGACAGTGTAATGGATGGTTCTCAGAACCATTTTACCACGAGA 300  
QY 301 CAGCCTGTTCTATCCTGTTTAAATAAATTAGTTTGGGTTCTCTACATGATTAACAACCC 360  
Db 301 CAGCCTGTTCTATCCTGTTTAAATAAATTAGTTTGGGTTCTCTACATGATTAACAACCC 360  
QY 361 TGCTCCCAATCTGTCACATAAAAGTCTGTGACTTTGAAGTTTGTAGTCAGCACCCCCACCACAAAC 420  
Db 361 TGCTCCCAATCTGTCACATAAAAGTCTGTGACTTTGAAGTTTGTAGTCAGCACCCCCACCACAAAC 420  
QY 421 TTTATTTTTCATGTGTTTGGCAACATATGAGTGTGTTTGAATAAAGTACCACATGTC 480  
Db 421 TTTATTTTTCATGTGTTTGGCAACATATGAGTGTGTTTGAATAAAGTACCACATGTC 480  
QY 481 TTTA 484  
Db |||||  
QY 481 TTTA 484  
RESULT 4  
AAH85083  
ID AAH85083 standard; cDNA; 484 BP.  
XX  
AC AAH85083;  
XX  
DT 25-SEP-2001 (first entry)  
XX  
DE Human prostate-specific cDNA sequence 22595.  
XX  
KW Human; prostate cancer; therapy; diagnosis; cat eye syndrome;  
KW chromosome 22q11.2; prostate-specific protein; chromosome 1;  
KW prostate specific antigen; PSA; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200134802-A2.  
XX  
PD 17-MAY-2001.  
XX  
PF 09-NOV-2000; 2000WO-US30904.  
XX  
PR 12-NOV-1999; 99US-0439313.  
PR 18-NOV-1999; 99US-0443686.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;  
PI Kalos MD, Retter MW, Stolk JA, Day CH, Skelky YAW, Wang A;  
XX

DR WPI; 2001-308785/32.  
 XX Isolated polypeptide comprising at least an immunogenic portion of a  
 PT prostate-specific protein, useful in the diagnosis and therapy of a  
 PT prostate cancer -  
 XX  
 PS  
 PS Claim 5; Page 273; 325pp; English.  
 XX  
 XX The present invention describes an isolated polypeptide (P1) comprising  
 CC at least an immunogenic portion of a prostate-specific protein, or its  
 CC variant. Also described are polynucleotides (N1) encoding (P1), or its  
 CC (N1) have cytostatic activity and can be used in vaccine production.  
 CC The polypeptides, nucleic acids and antibodies from the present  
 CC invention are useful in the diagnosis and therapy of prostate cancer.  
 CC Prostate specific genes P704P, P712P, P774P, P775P and B305D are located  
 CC in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome  
 CC region. Prostate specific antigen (PSA) P501S was located on  
 CC chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent  
 CC polynucleotide and polypeptide sequences used in the exemplification  
 CC of the present invention.  
 XX  
 XX Sequence 484 BP; 137 A; 101 C; 73 G; 173 T; 0 other;

Query Match 100.0%; Score 484; DB 22; Length 484;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-116;  
 Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTTTAAATAAGCATTTAGTCTCAGTCCCTACTGAGTACHTCTTCTCCCTCTCTG 60  
 Db 1 TTTTAAATAAGCATTTAGTCTCAGTCCCTACTGAGTACHTCTTCTCCCTCTCTG 60  
 QY 61 AATTTAAATCTTCAACTGCAATTTGCAAGGATTACACATTTCACTGTGATGATATG 120  
 Db 61 AATTTAAATCTTCAACTGCAATTTGCAAGGATTACACATTTCACTGTGATGATATG 120  
 QY 121 TGTTCGCAAAAAAAGAGTCTTCTTTTAAATTAATTTGTTTGTGAATCATCTTGC 180  
 Db 121 TGTTCGCAAAAAAAGAGTCTTCTTTTAAATTAATTTGTTTGTGAATCATCTTGC 180  
 QY 181 TTTTTCCTCCATTTGAAGTCTGATTAACCCATCTCTGAAGTGTGAGAAACATCTGAAG 240  
 Db 181 TTTTTCCTCCATTTGAAGTCTGATTAACCCATCTCTGAAGTGTGAGAAACATCTGAAG 240  
 QY 241 AGCTAGTCTATCAGCATCTGACAGGTGAATTTGATGTTTCTCAGAACCATTTCCACCAGA 300  
 Db 241 AGCTAGTCTATCAGCATCTGACAGGTGAATTTGATGTTTCTCAGAACCATTTCCACCAGA 300  
 QY 301 CAGCCTGTTTCTATCTCTGTTTAAATTAATTTGTTTGTGAATCATCTTGC 180  
 Db 301 CAGCCTGTTTCTATCTCTGTTTAAATTAATTTGTTTGTGAATCATCTTGC 180  
 QY 361 TGCTCCAACTGTCACATAAAAGTCTGTGACATTTGATGTTTGTGAATCATCTTGC 180  
 Db 361 TGCTCCAACTGTCACATAAAAGTCTGTGACATTTGATGTTTGTGAATCATCTTGC 180  
 QY 421 TTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATTAAGTACCCATGTC 480  
 Db 421 TTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATTAAGTACCCATGTC 480  
 QY 481 TTTA 484  
 Db 481 TTTA 484

RESULT 5  
 AAH02834  
 ID AAH02834 standard; cDNA; 484 BP.  
 XX  
 AC AAH02834;  
 XX  
 DT 14-JUN-2001 (first entry)  
 XX  
 DE Prostate tumour antigen cDNA sequence for 22595.

XX Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;  
 KW prostate cancer; immunogenic; cytostatic; vaccine; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200125272-A2.  
 XX  
 PD 12-APR-2001.  
 XX  
 PF 04-OCT-2000; 2000WO-US27464.  
 XX  
 PR 04-OCT-1999; 99US-0157455.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Xu J, Skelky YAW, Reed SG, Cheever MA;  
 XX WPI; 2001-245062/25.  
 DR  
 XX Prostate specific protein and its encoding polynucleotide, useful for  
 PT the treatment and diagnosis of prostate cancer -  
 PT  
 XX Claim 4; Page 256; 276pp; English.  
 PS  
 PS The present invention describes an isolated polypeptide (I) comprising  
 CC at least an immunogenic portion of a prostate tumour antigen protein or  
 CC its variant. (I) have cytostatic activity and can be used in vaccine  
 CC production. (I), prostate tumour antigen polynucleotides, an antigen  
 CC presenting cell (APC e.g. a dendritic cell) that expresses (I), and a  
 CC pharmaceutical composition containing (I) are useful for inhibiting the  
 CC development of cancer in a patient. Antibodies specific for prostate  
 CC specific proteins and oligonucleotides that hybridize to a  
 CC polynucleotide that encodes a prostate specific protein are useful  
 CC for detecting the presence or absence of a cancer or monitoring the  
 CC progression the progression of a cancer, especially prostate cancer.  
 CC AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences  
 CC used in the exemplification of the present invention.  
 XX  
 XX Sequence 484 BP; 137 A; 101 C; 73 G; 173 T; 0 other;  
 SQ  
 Query Match 100.0%; Score 484; DB 22; Length 484;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-116;  
 Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTTTAAATAAGCATTTAGTCTCAGTCCCTACTGAGTACTTCTCTCCCTCTCTG 60  
 Db 1 TTTTAAATAAGCATTTAGTCTCAGTCCCTACTGAGTACTTCTCTCCCTCTCTG 60  
 QY 61 AATTTAAATCTTCAACTGCAATTTGCAAGGATTACACATTTCACTGTGATGATATG 120  
 Db 61 AATTTAAATCTTCAACTGCAATTTGCAAGGATTACACATTTCACTGTGATGATATG 120  
 QY 121 TGTTCGCAAAAAAAGAGTCTTCTTTTAAATTAATTTGTTTGTGAATCATCTTGC 180  
 Db 121 TGTTCGCAAAAAAAGAGTCTTCTTTTAAATTAATTTGTTTGTGAATCATCTTGC 180  
 QY 181 TTTTTCCTCCATTTGAAGTCTGATTAACCCATCTCTGAAGTGTGAGAAACATCTGAAG 240  
 Db 181 TTTTTCCTCCATTTGAAGTCTGATTAACCCATCTCTGAAGTGTGAGAAACATCTGAAG 240  
 QY 241 AGCTAGTCTATCAGCATCTGACAGGTGAATTTGATGTTTCTCAGAACCATTTCCACCAGA 300  
 Db 241 AGCTAGTCTATCAGCATCTGACAGGTGAATTTGATGTTTCTCAGAACCATTTCCACCAGA 300  
 QY 301 CAGCCTGTTTCTATCTCTGTTTAAATTAATTTGTTTGTGAATCATCTTGC 180  
 Db 301 CAGCCTGTTTCTATCTCTGTTTAAATTAATTTGTTTGTGAATCATCTTGC 180  
 QY 361 TGCTCCAACTGTCACATAAAAGTCTGTGACATTTGATGTTTGTGAATCATCTTGC 180  
 Db 361 TGCTCCAACTGTCACATAAAAGTCTGTGACATTTGATGTTTGTGAATCATCTTGC 180  
 QY 421 TTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATTAAGTACCCATGTC 480  
 Db 421 TTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATTAAGTACCCATGTC 480  
 QY 481 TTTA 484  
 Db 481 TTTA 484

Qy 421 TTTATTTTCTATGTGTTTTTGCACATATGAGTGTGTTTGAATAAAGTACCCATGTC 480  
Db 421 TTTATTTTCTATGTGTTTTTGCACATATGAGTGTGTTTGAATAAAGTACCCATGTC 480  
Qy 481 TTTA 484  
Db 481 TTTA 484

RESULT 6

ABL95233  
ID ABL95233 standard; cDNA; 484 BP.  
XX AC ABL95233;

DT 19-JUL-2002 (first entry)

DE Human 22595 cDNA sequence SEQ ID NO 434.

XX Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;  
KW gene therapy; gene; ss.

OS Homo sapiens.

XX US2002022248-A1.

PN 21-FEB-2002.

PD 12-JAN-2001; 2001US-0759143.

PR 25-FEB-1997; 97US-0806099.

PR 01-AUG-1997; 97US-0904804.

PR 09-FEB-1998; 98US-0020956.

PR 25-FEB-1998; 98US-0030607.

PR 14-JUL-1998; 98US-0115453.

PR 23-SEP-1998; 98US-0159812.

PR 15-JAN-1999; 99US-0232149.

PR 09-APR-1999; 99US-0288946.

PR 13-JUL-1999; 99US-0352616.

PR 12-NOV-1999; 99US-0439313.

PR 18-NOV-1999; 99US-0443686.

PR 14-JAN-2000; 2000US-0483672.

PR 27-MAR-2000; 2000US-0536857.

PR 09-MAY-2000; 2000US-0568100.

PR 12-MAY-2000; 2000US-0570737.

PR 13-JUN-2000; 2000US-0593793.

PR 27-JUN-2000; 2000US-0605783.

PR 10-AUG-2000; 2000US-0636215.

PR 29-AUG-2000; 2000US-0651236.

PR 06-SEP-2000; 2000US-0657279.

PR 02-OCT-2000; 2000US-0679426.

PR 10-OCT-2000; 2000US-0685166.

XX (XUJJ/) XU J.

PA (DILL/) DILLON D C.

PA (MITC/) MITCHAM J L.

PA (HARL/) HARLOCKER S L.

PA (JIAN/) JIANG Y.

PA (KALO/) KALOS M D.

PA (FANG/) FANGER G R.

PA (RETT/) RETTER M W.

PA (STOL/) STOLK J A.

PA (DAYC/) DAY C H.

PA (VEDV/) VEDVICK T S.

PA (CART/) CARTER D.

PA (LISX/) LI S X.

PA (WANG/) WANG A.

PA (SKEI/) SKEIKY Y A W.

PA (HEPL/) HEPLER W T.

PA (HEND/) HENDERSON R A.

XX Xu J, Dillon DC, Harlocker SL, Jiang Y, Kalos MD;  
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;

PI

XX Li SX, Wang A, Skelky YAW, Hepler WT, Henderson RA;

XX WPI; 2002-255649/30.

XX New prostate-specific polynucleotides for diagnosing and treating  
PT diseases, in particular prostate cancer, and as markers for the  
PT progression of cancer -

XX PS Claim 1; SEQ ID NO 434; 87pp; English.

XX The present invention provides prostate-specific coding sequences and  
CC their encoded proteins. These can be used in the diagnosis and treatment  
CC of cancers, particularly prostate cancer. The present sequence is a cDNA  
CC described in the invention.

XX SQ Sequence 484 BP; 137 A; 101 C; 73 G; 173 T; 0 other;

Query Match 100.0%; Score 484; DB 24; Length 484;

Best Local Similarity 100.0%; Pred. No. 1.4e-116;

Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTAAATAAGCATTTAGTGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCCTG 60

Db 1 TTTTAAATAAGCATTTAGTGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCCTG 60

Qy 61 AATTAAATCTTTCACACTTGCAGTTCGAAGGATTACACATTTTCACTGTGATATATG 120

Db 61 AATTAAATCTTTCACACTTGCAGTTCGAAGGATTACACATTTTCACTGTGATATATG 120

Qy 121 TGTGCAAAAAAAGAGTCTTTGTTTAAATTAATTTGTTGGTTTGAATCCATCTGC 180

Db 121 TGTGCAAAAAAAGAGTCTTTGTTTAAATTAATTTGTTGGTTTGAATCCATCTGC 180

Qy 181 TTTTCCCATTTGGAAGTCTTTGTTTAAATTAATTTGTTGGTTTGAATCCATCTGC 240

Db 181 TTTTCCCATTTGGAAGTCTTTGTTTAAATTAATTTGTTGGTTTGAATCCATCTGC 240

Qy 241 AGCTAGTCTATCAGCATCTGACAGGTGAATTTGATGTTTCTCAGAACCATTTCACCCAGA 300

Db 241 AGCTAGTCTATCAGCATCTGACAGGTGAATTTGATGTTTCTCAGAACCATTTCACCCAGA 300

Qy 301 CAGCCTGTTTCTATCCTGTTTAAATAAATTAATTTGTTGGTTTCTACATGATCAACACC 360

Db 301 CAGCCTGTTTCTATCCTGTTTAAATAAATTAATTTGTTGGTTTCTACATGATCAACACC 360

Qy 361 TGCTCCAATCTGTCACATAAAGTCTGTGACTTGAAGTTTAGTCAGCACCCCCACCAAC 420

Db 361 TGCTCCAATCTGTCACATAAAGTCTGTGACTTGAAGTTTAGTCAGCACCCCCACCAAC 420

Qy 421 TTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATAAATTAAGTACCCATGTC 480

Db 421 TTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATAAATTAAGTACCCATGTC 480

Qy 481 TTTA 484

Db 481 TTTA 484

RESULT 7

ACA59670

ID ACA59670 standard; cDNA; 484 BP.

XX ACA59670;

XX 10-JUN-2003 (first entry)

XX Prostate cancer therapy associated cDNA #413.

XX Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;  
KW immunogen; cancer; prostate specific antigen; PSA;  
KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;  
KW PSMA; gene; ss.

OS Homo sapiens.  
 XX US2002192763-A1.  
 PN 19-DEC-2002.  
 PD 29-JUN-2001; 2001US-0895793.  
 XX 17-APR-2000; 2000US-157455P.  
 PR 04-OCT-2000; 2000US-0679272.  
 PR 28-MAR-2001; 2001US-0822827.  
 XX (XUJJ/) XU J.  
 PA (DILL/) DILLON D C.  
 PA (MITC/) MITCHAM J L.  
 PA (HARL/) HARLOCKER S L.  
 PA (JIAN/) JIANG Y.  
 PA (KALO/) KALOS M D.  
 PA (FANG/) FANGER G R.  
 PA (RETT/) RETTER M W.  
 PA (STOL/) STOLK J A.  
 PA (DAYC/) DAY C H.  
 PA (VEDV/) VEDVICK T S.  
 PA (CART/) CARTER D.  
 PA (LISX/) LI S X.  
 PA (WANG/) WANG A.  
 PA (SKEL/) SKEIKY Y A W.  
 PA (HEPL/) HEPLER W T.  
 PA (HEND/) HENDERSON R A.  
 PA (HURA/) HURAL J.  
 PA (MCNE/) MCNEILL P D.  
 PA (HOUG/) HOUGHTON R L.  
 PA (DBAS/) Y DE BASSOLS C V.  
 PA (FOYT/) FOY T M.  
 XX  
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;  
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;  
 PI Li SX, Wang A, Skeiky YAW Hepler WT, Henderson RA, Hural J;  
 PI McNeill PD, Houghton RL, Y De Bassols CV, Foy TM;  
 DR WPI; 2003-352711/33.  
 XX  
 PT New fusion protein comprising prostate-specific polypeptides, or its  
 PT immunogenic portions, useful for diagnosing, preventing and/or treating  
 PT cancer, particularly prostate cancer.  
 XX  
 PS Example 14; SEQ ID NO 434; 85pp; English.  
 CC The invention describes a fusion protein comprising at least one amino  
 CC acid sequence of immunogenic portions of any of the 3 sequences not  
 CC defined in the specification, or sequences having at least 70 or 90 %  
 CC sequence identity to any one of the 35 sequences defined in the USPTO  
 CC web site, which is encoded by any of the 4 nucleotide sequences not  
 CC defined in the specification. The fusion protein, composition and  
 CC methods are useful for diagnosing, preventing and/or treating cancer,  
 CC particularly prostate cancer. The proteins are useful as markers to  
 CC indicate the presence or absence of cancer. This sequence  
 CC represents a prostate cancer therapy associated cDNA.  
 CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from the US patent office at  
 CC seqdata.uspto.gov/sequence.html?DocID=US20020192763.  
 XX  
 SQ Sequence 484 BP; 137 A; 101 C; 73 G; 173 T; 0 other;  
 Query Match 100.0%; Score 484; DB 25; Length 484;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-116;  
 Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTTTAAATAAGCATTTAGTCTCCTACTGAGTACTCTTCTCTCCCTCCCTCTG 60  
 DB 1 TTTTAAATAAGCATTTAGTCTCCTACTGAGTACTCTTCTCTCCCTCCCTCTG 60

QY 61 AATTAAATCTTTCAACTTGCAGGATTACACATTTCACTGTGATATTTG 120  
 DB |||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 61 AATTAAATCTTTCAACTTGCAGGATTACACATTTCACTGTGATATTTG 120  
 DB |||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 121 TGTGCAAAAAAAGTGTCTTTGTTTAAATTAATTTGTTGTTGTAATCCATCTTGC 180  
 DB |||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 121 TGTGCAAAAAAAGTGTCTTTGTTTAAATTAATTTGTTGTTGTAATCCATCTTGC 180  
 DB |||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 181 TTTTCCCATTTGGAACTAGTCAATTAACCCATCTCTGAACCTGGTAGAAAAACATCTGAAG 240  
 DB |||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 181 TTTTCCCATTTGGAACTAGTCAATTAACCCATCTCTGAACCTGGTAGAAAAACATCTGAAG 240  
 DB |||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 241 AGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGTTCTCAGAACATTTTCCACCAGA 300  
 DB |||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 241 AGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGTTCTCAGAACATTTTCCACCAGA 300  
 DB |||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 301 CAGCCTGTTCTATCTCTTTTAAATAATTTAGTTTGGGTTCTCTACATGCATACAAACCC 360  
 DB |||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 301 CAGCCTGTTCTATCTCTTTTAAATAATTTAGTTTGGGTTCTCTACATGCATACAAACCC 360  
 DB |||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 361 TGCTCCAAATCTGCACATAAAAGTCTGACCTTGAAGTTTAGTCAGACCCCAACCAAC 420  
 DB |||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 361 TGCTCCAAATCTGCACATAAAAGTCTGACCTTGAAGTTTAGTCAGACCCCAACCAAC 420  
 DB |||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 421 TTTATTTTCTATGTTGTTTTCACATATAGTGTGTTTGAATAAATAGTATCCCATGTC 480  
 DB |||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 421 TTTATTTTCTATGTTGTTTTCACATATAGTGTGTTTGAATAAATAGTATCCCATGTC 480  
 DB |||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 481 TTTA 484  
 DB |||||  
 QY 481 TTTA 484  
 DB |||||  
 RESULT 8  
 AAF15823  
 ID AAF15823 standard; cDNA; 755 BP.  
 XX  
 AC AAF15823;  
 XX  
 DT 13-MAR-2001 (first entry)  
 XX  
 DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:258.  
 XX  
 KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;  
 KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;  
 KW vulnary; gastrointestinal; nephrotropic; antiinfective; gynaecological;  
 KW antibacterial; gene therapy; neural; immune; reproductive; renal;  
 KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;  
 KW wound; infectious disease; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200055174-A1.  
 PD 21-SEP-2000.  
 XX  
 PF 08-MAR-2000; 2000WO-US05988.  
 XX  
 PR 12-MAR-1999; 99US-0124270.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (ROSE/) ROSEN C A.  
 XX  
 PI Rosen CA, Ruben SM;  
 XX  
 DR WPI; 2000-587513/55.  
 DR P-PSDB; AAB56620.  
 XX  
 PT Prostate cancer associated gene sequences, referred to as prostate  
 PT cancer antigens, useful for treatment, prevention, and diagnosis of  
 PT disorders such as prostate cancer.  
 XX  
 PS Claim 1; Page 781; 2338pp; English.



Db 434 ACTTTATTTTCTATGTGTTTTTTTGAACATATGAGTCTTTTGAATAAAGTACCATG 375

Qy 479 TCTTTA 484  
|||||

Db 374 TCTTTA 369

RESULT 10  
AAA06564  
ID AAA06564 standard; cDNA; 2984 BP.  
XX AC AAA06564;  
XX  
XX 13-JUN-2000 (first entry)  
XX  
DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:335.  
XX KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;  
XX KW immunogenic; cytostatic; vaccine; ss.  
XX OS Homo sapiens.  
XX  
XX PN WO200004149-A2.  
XX  
XX PD 27-JAN-2000.  
XX  
XX 14-JUL-1999; 99WO-US15838.  
XX PF  
XX PR 14-JUL-1998; 98US-0115453.  
XX PR 14-JUL-1998; 98US-0116134.  
XX PR 23-SEP-1998; 98US-0159812.  
XX PR 23-SEP-1998; 98US-0159822.  
XX PR 15-JAN-1999; 99US-0232149.  
XX PR 15-JAN-1999; 99US-0232880.  
XX PR 09-APR-1999; 99US-0288946.  
XX  
XX PA (CORI-) CORIXA CORP.  
XX  
XX PI Dillon DC, Harlocker SL, Yugiu J, Xu J, Mitcham JL;  
XX WPI; 2000-171268/15.  
XX  
XX  
XX PT New polypeptide useful for treating and diagnosing prostate cancer  
XX PT comprises an immunogenic portion of prostate tumor protein -  
XX PS Claim 50; Page 207-208; 263pp; English.  
XX  
XX CC The present invention describes isolated polypeptides, comprising an  
XX CC immunogenic portion of a prostate tumour protein (PTP). The polypeptides  
XX CC and polynucleotides encoding them have cytostatic activity and can be  
XX CC used in vaccines and in gene therapy. The polypeptides and  
XX CC polynucleotides encoding them, antigen presenting cells which express  
XX CC the polypeptides, antibodies against the polypeptides and vaccines  
XX CC comprising them can be used for inhibiting the development of prostate  
XX CC cancer in a patient. The polypeptides can be used to generate antibodies  
XX CC or anti-idiotypic antibodies for passive immuno therapy. A portion of  
XX CC the polynucleotides encoding the polypeptides can be used as a probe or  
XX CC to modulate the expression of the polypeptides. AAA06241 to AAA06691 and  
XX CC AAY82000 to AAY82020 represent sequences used in the exemplification of  
XX CC the present invention.  
XX  
XX SQ Sequence 2984 BP; 837 A; 659 C; 645 G; 842 T; 1 other;  
Query Match 97.5%; Score 472; DB 21; Length 2984;  
Best Local Similarity 99.6%; Pred. No. 3,2e-113;  
Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;  
Qy 1 TTTTAAATAAGCATTTAGTGTCTAGTCCCTACTGACTCTTTCTCTCCCTCCCTCTG 60  
Db 2473 TTTTAAATAAGCATTTAGTGTCTAGTCCCTACTGACTCTTTCTCTCCCTCCCTCTG 2532  
Qy 61 AATTAAATCTTTCAACTTGAATTTGAAGSATTACACATTTCACGTGATGATATG 120  
|||||

```

XX PS Claim 1; Page 335-336; 579pp; English.
XX CC The invention relates to isolated prostate-specific
XX CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
XX CC antibodies raised against the polypeptides (or antigenic epitopes
XX CC derived from them) and antigen-presenting cells expressing the
XX CC polypeptides. The antibodies are useful for detecting the presence of
XX CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
XX CC the antigen-presenting cells are useful for stimulating and/or expanding
XX CC T cells specific for a tumour protein, and for inhibiting the development
XX CC of cancer especially prostate cancer. Compositions comprising the
XX CC polynucleotide and/or polypeptide are useful for stimulating an immune
XX CC response, and for treating cancer. The oligonucleotide is useful for
XX CC detecting cancer. The present sequence is a prostate specific
XX CC polynucleotide of the invention.
XX SQ Sequence 2984 BP; 837 A; 659 C; 645 G; 842 T; 1 other;

Query Match          97.5%; Score 472; DB 22; Length 2984;
Best Local Similarity 99.6%; Pred. No. 3.2e-113;
Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy 1 TTTTAAATAAGCAATTTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTG 60
Dy 2473 TTTTAAATAAGCAATTTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTG 2532
Qy 61 AATTTAATCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATATATG 120
Dy 2533 AATTTAATCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATATATG 2592
Qy 121 TGTGTC--AAAAAAGTGTCTTTGTTTAAATTTACTTGGTTGTGAATCCATCTT 178
Dy 2593 TGTGTC--AAAAAAGTGTCTTTGTTTAAATTTACTTGGTTGTGAATCCATCTT 2652
Qy 179 GCTTTTCCCAATTTGGAAGTGTCTTTAAACCCATCTCTGAACTGTGATAAATCTGA 238
Dy 2653 GCTTTTCCCAATTTGGAAGTGTCTTTAAACCCATCTCTGAACTGTGATAAATCTGA 2712
Qy 239 AGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGGTCTCAGAACCAATCTGA 298
Dy 2713 AGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGGTCTCAGAACCAATCTGA 298
Qy 299 GACAGCCTGTTTCTATCTCTGTTTAAATTTAGTTGGTCTCTACATGATGATATATG 358
Dy 2773 GACAGCCTGTTTCTATCTCTGTTTAAATTTAGTTGGTCTCTACATGATGATATATG 358
Qy 479 TCTTTA 484
Dy 2953 TCTTTA 2958

RESULT 12
AAH93680
ID AAH93680 standard; cDNA; 2984 BP.
XX AC AAH93680;
XX AC AAH93680;
XX DF 04-OCT-2001 (first entry)
XX DE Human prostate-specific cDNA sequence p705P.
XX KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
XX KW cytostatic; gene therapy; metastasis; ss.
XX
```

```

OS Homo sapiens.
XX PN WO200151633-A2.
XX PD 19-JUL-2001.
XX PF 16-JAN-2001; 2001WO-US01574.
XX PR 14-JAN-2000; 2000US-0483672.
XX PA (CORI-) CORIXA CORP.
XX PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Meagher MJ;
XX WPI; 2001-425873/45.
XX New polynucleotide encoding a prostate-specific protein, for
XX diagnosing, monitoring and treating prostate cancer in a patient and
XX for use in vaccines -
XX Claim 1; Page 333-334; 543pp; English.
XX The present invention describes polynucleotide sequences (I) which encode
XX prostate-specific proteins (II). (I) and (II) have cytostatic activity,
XX and can be used in vaccine production and gene therapy. (I), (II),
XX antibodies to (II), fusion proteins comprising (II), and isolated
XX T cells prepared using (I) or (II) are used in the detection of cancer in a
XX patient. The cancer that is diagnosed or treated is particularly
XX prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
XX (I) and (II) can also be used to improve diagnostic and therapeutic
XX methods for prostate cancer. They can indicate the level of metastasis
XX as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
XX AAH01318 represent polynucleotide and amino acid sequences used in the
XX exemplification of the present invention.
XX SQ Sequence 2984 BP; 837 A; 659 C; 645 G; 842 T; 1 other;

Query Match          97.5%; Score 472; DB 22; Length 2984;
Best Local Similarity 99.6%; Pred. No. 3.2e-113;
Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy 1 TTTTAAATAAGCAATTTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTG 60
Dy 2473 TTTTAAATAAGCAATTTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTG 2532
Qy 61 AATTTAATCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATATATG 120
Dy 2533 AATTTAATCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATATATG 2592
Qy 121 TGTGTC--AAAAAAGTGTCTTTGTTTAAATTTACTTGGTTGTGAATCCATCTT 178
Dy 2593 TGTGTC--AAAAAAGTGTCTTTGTTTAAATTTACTTGGTTGTGAATCCATCTT 2652
Qy 179 GCTTTTCCCAATTTGGAAGTGTCTTTAAACCCATCTCTGAACTGTGATAAATCTGA 238
Dy 2653 GCTTTTCCCAATTTGGAAGTGTCTTTAAACCCATCTCTGAACTGTGATAAATCTGA 2712
Qy 239 AGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGGTCTCAGAACCAATCTGA 298
Dy 2713 AGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGGTCTCAGAACCAATCTGA 298
Qy 299 GACAGCCTGTTTCTATCTCTGTTTAAATTTAGTTGGTCTCTACATGATGATATATG 358
Dy 2773 GACAGCCTGTTTCTATCTCTGTTTAAATTTAGTTGGTCTCTACATGATGATATATG 358
Qy 359 CCTGCTCAATCTGTACATATAAAGTGTCTGACTGTGAATTTAGTTGGATGATATATG 418
Dy 2833 CCTGCTCAATCTGTACATATAAAGTGTCTGACTGTGAATTTAGTTGGATGATATATG 418
XX
```

```

QY 419 ACTTATTTTCTATGCTGTTTTTGCACATATAGAGTCTTTGAAATAAAGTACCCATG 478
Db 2893 ACTTATTTTCTATGCTGTTTTTGCACATATAGAGTCTTTGAAATAAAGTACCCATG 2952
QY 479 TCTTTTA 484
Db 2953 TCTTTTA 2958

RESULT 13
AAH84994
ID AAH84994 standard; cDNA; 2984 BP.
AC AAH84994;
XX
XX
XX 25-SEP-2001 (first entry)
XX
DE Human prostate-specific cDNA sequence P705P/9-F3.
XX
KW Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
KW chromosome 22q11.2; prostate-specific protein; chromosome 1;
KW prostate specific antigen; PSA; ss.
XX
OS Homo sapiens.
XX
XX WO200134802-A2.
XX
XX 17-MAY-2001.
XX
XX 09-NOV-2000; 2000WO-US30904.
XX
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
XX Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAW, Wang A;
XX WPI; 2001-308785/32.
XX
XX Isolated polypeptide comprising at least an immunogenic portion of a
XX prostate-specific protein, useful in the diagnosis and therapy of
XX prostate cancer -
XX
XX Claim 31; Page 233-234; 325pp; English.
XX
XX The present invention describes an isolated polypeptide (P1) comprising
XX at least an immunogenic portion of a prostate-specific protein, or its
XX variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
XX (N1) have cytostatic activity and can be used in vaccine production.
XX The polypeptides, nucleic acids and antibodies from the present
XX invention are useful in the diagnosis and therapy of prostate cancer.
XX Prostate specific genes P704P, P712P, P774P, P775P and B305D are located
XX in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome
XX region. Prostate specific antigen (PSA) P501S was located on
XX chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent
XX polynucleotide and polypeptide sequences used in the exemplification
XX of the present invention.
XX
XX Sequence 2984 BP; 837 A; 659 C; 645 G; 842 T; 1 other;
XX
XX Query Match 97.5%; Score 472; DB 22; Length 2984;
XX Best Local Similarity 99.6%; Pred. No. 3.2e-113;
XX Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
XX
XX 1 TTTTAAATAAGCATTTAGTCTCAGTCCCTACTGAGTACTCTTCTCTCCCTCTCTCTG 60
XX
XX 2473 TTTTAAATAAGCATTTAGTCTCAGTCCCTACTGAGTACTCTTCTCTCCCTCTCTG 2532
XX
XX 61 AATTATATCTTCAACTGCAATTGCAAGGATTACACATTTCACTGTGATGATATG 120
XX
XX 2533 AATTATATCTTCAACTGCAATTGCAAGGATTACACATTTCACTGTGATGATATG 2592
XX

```

```

QY 121 TGTTGC--AAAAAAGTGTCTTTGTTTAAAAATTACTTGGTTTGTGAATCCATCTT 178
Db 2593 TGTTGCAAAAAAAGTGTCTTTGTTTAAAAATTACTTGGTTTGTGAATCCATCTT 2652
QY 179 GCTTTTCCCATTTGGAAGTGTCTTAAACCATCTCTGAACTGGTAGAAAAACATCTGA 238
Db 2653 GCTTTTCCCATTTGGAAGTGTCTTAAACCATCTCTGAACTGGTAGAAAAACATCTGA 2712
QY 239 AGAGCTAGTCTATCAGCATCTGACAGGTGAATTGGATGGTTCTCAGAACATTTTCACCCA 298
Db 2713 AGAGCTAGTCTATCAGCATCTGACAGGTGAATTGGATGGTTCTCAGAACATTTTCACCCA 2772
QY 299 GACAGCCTGTTTCTATCTCTGTTTAAATAATTAATTAATTAATTAATTAATTAATTAAT 358
Db 2773 GACAGCCTGTTTCTATCTCTGTTTAAATAATTAATTAATTAATTAATTAATTAATTAAT 2832
QY 359 CCTGCTCCAATCTGCATATAAAAGTCTGTGACTTGAAGTTTGTAGTCAGCAGCCCCCACCAC 418
Db 2833 CCTGCTCCAATCTGCATATAAAAGTCTGTGACTTGAAGTTTGTAGTCAGCAGCCCCCACCAC 2892
QY 419 ACTTTATTTTCTATGCTGTTTTTGTGCAACATATGAGTGTGTTTGAATAAAGTACCCATG 478
Db 2893 ACTTTATTTTCTATGCTGTTTTTGTGCAACATATGAGTGTGTTTGAATAAAGTACCCATG 2952
QY 479 TCTTTTA 484
Db 2953 TCTTTTA 2958

RESULT 14
AAH02745
ID AAH02745 standard; cDNA; 2984 BP.
XX
XX AC AAH02745;
XX
XX 14-JUN-2001 (first entry)
XX
XX Prostate tumour antigen determined cDNA sequence for P705P.
XX
XX Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;
XX prostate cancer; immunogenic; cytostatic; vaccine; ss.
XX
XX Homo sapiens.
XX
XX WO200125272-A2.
XX
XX 12-APR-2001.
XX
XX 04-OCT-2000; 2000WO-US27464.
XX
XX 04-OCT-1999; 99US-0157455.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Skeiky YAW, Reed SG, Cheever MA;
XX WPI; 2001-245062/25.
XX
XX P-PSDB; AAB74809.
XX
XX Prostate specific protein and its encoding polynucleotide, useful for
XX the treatment and diagnosis of prostate cancer -
XX
XX Claim 50; Page 219; 276pp; English.
XX
XX The present invention describes an isolated polypeptide (I) comprising
XX at least an immunogenic portion of a prostate tumour antigen protein or
XX its variant. (I) have cytostatic activity and can be used in vaccine
XX production. (I), prostate tumour antigen polynucleotides, an antigen
XX presenting cell (APC e.g. a dendritic cell) that expresses (I), and a
XX pharmaceutical composition containing (I) are useful for inhibiting the
XX development of cancer in a patient. Antibodies specific for prostate
XX specific proteins and oligonucleotides that hybridise to a

```



CC polynucleotide that encodes a prostate specific protein are useful  
 CC for detecting the presence or absence of a cancer or monitoring the  
 CC progression the progression of a cancer, especially prostate cancer.  
 CC AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences  
 CC used in the exemplification of the present invention.

XX  
 SQ Sequence 2984 BP; 837 A; 659 C; 645 G; 842 T; 1 other;

Query Match 97.5%; Score 472; DB 22; Length 2984;  
 Best Local Similarity 99.6%; Pred. No. 3.2e-113;  
 Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 TTTTAAATTAAGCATTTAGTGCCTCAGTCCCTACTGAGTACTCTTCTCCTCCCTCCTCTG 60  
 DB 2473 TTTTAAATTAAGCATTTAGTGCCTCAGTCCCTACTGAGTACTCTTCTCCTCCCTCCTCTG 2532  
 QY 61 AATTTAATTTCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATGATATG 120  
 DB 2533 AATTTAATTTCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATGATATG 2592  
 QY 121 TGTGTC--AAAAAATAAGTCTCTTGTGTTTAAATTAATTTGTTGTAATCCATCTT 178  
 DB 2593 TGTGTC--AAAAAATAAGTCTCTTGTGTTTAAATTAATTTGTTGTAATCCATCTT 2652  
 QY 179 GCTTTTCCCATTTGCAATTTGCAAGGATTACACATTTCACTGTGATGATATG 238  
 DB 2653 GCTTTTCCCATTTGCAATTTGCAAGGATTACACATTTCACTGTGATGATATG 2712  
 QY 239 AGAGCTAGTCTATCAGCATCTGACAGTGAATTTGGATGTTCTCAGAACCATTTCA 298  
 DB 2713 AGAGCTAGTCTATCAGCATCTGACAGTGAATTTGGATGTTCTCAGAACCATTTCA 2772  
 QY 299 GACAGCTGTTTCTATCCTCTTCTTAAATAAATTTAGTTGGTCTCTACATGCATAA 358  
 DB 2773 GACAGCTGTTTCTATCCTCTTCTTAAATAAATTTAGTTGGTCTCTACATGCATAA 2832  
 QY 359 CCTGCTCCAATCTGTCACATAAAGTCTGTGACTTTGAAGTTTGTAGTACAGACCC 418  
 DB 2833 CCTGCTCCAATCTGTCACATAAAGTCTGTGACTTTGAAGTTTGTAGTACAGACCC 2892  
 QY 419 ACTTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATAAAGTACCCATG 478  
 DB 2893 ACTTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATAAAGTACCCATG 2952  
 QY 479 TCTTTA 484  
 DB 2953 TCTTTA 2958

RESULT 15  
 AAF86953  
 ID AAF86953 standard; cDNA; 2984 BP.  
 XX AC AAF86953;  
 XX AC  
 XX 06-JUL-2001 (first entry)  
 DT  
 XX  
 DE Human P705P inventive antigen coding sequence SEQ ID NO: 349.  
 XX  
 KW Human; mouse; immunotherapy; cancer; leukaemia; WT1; Wilm's tumour gene;  
 KW chromosome 11p13; zinc finger transcription factor; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200125273-A2.  
 XX  
 PD 12-APR-2001.  
 XX  
 PF 04-OCT-2000; 2000WO-US27465.  
 XX  
 PR 04-OCT-1999; 99US-0157459.  
 XX  
 PA (CORI-) CORIXA CORP.

XX Skeiky YAW, Xu J, Cheever MA, Reed SG;  
 PI WPI; 2001-328324/34.  
 XX  
 DR Polypeptide comprising part of the wilm's tumour gene product sequence is  
 PT used in the diagnosis and treatment of malignant diseases e.g. leukemia  
 PT and cancer associated with WT1 -  
 XX  
 PS Disclosure; Page 221-222; 228pp; English.  
 XX  
 CC The present invention describes compositions comprising peptides derived  
 CC from the wilm's tumour protein WT1 and methods for their use in treating  
 CC malignant diseases. Peptides derived from both the murine and human WT1  
 CC proteins are provided. The human WT1 gene is found on chromosome 11p13,  
 CC and the protein was shown to be a zinc finger transcription factor. The  
 CC immunogenic peptides of the invention are particularly useful in the  
 CC diagnosis and treatment of cancer and leukaemia. The present sequence is  
 CC a coding sequence used in the exemplification of the invention.

XX  
 SQ Sequence 2984 BP; 837 A; 659 C; 645 G; 842 T; 1 other;

Query Match 97.5%; Score 472; DB 22; Length 2984;  
 Best Local Similarity 99.6%; Pred. No. 3.2e-113;  
 Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 TTTTAAATTAAGCATTTAGTGCCTCAGTCCCTACTGAGTACTCTTCTCCTCCCTCCTCTG 60  
 DB 2473 TTTTAAATTAAGCATTTAGTGCCTCAGTCCCTACTGAGTACTCTTCTCCTCCCTCCTCTG 2532  
 QY 61 AATTTAATTTCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATGATATG 120  
 DB 2533 AATTTAATTTCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATGATATG 2592  
 QY 121 TGTGTC--AAAAAATAAGTCTCTTGTGTTTAAATTAATTTGTTGTAATCCATCTT 178  
 DB 2593 TGTGTC--AAAAAATAAGTCTCTTGTGTTTAAATTAATTTGTTGTAATCCATCTT 2652  
 QY 179 GCTTTTCCCATTTGCAATTTGCAAGGATTACACATTTCACTGTGATGATATG 238  
 DB 2653 GCTTTTCCCATTTGCAATTTGCAAGGATTACACATTTCACTGTGATGATATG 2712  
 QY 239 AGAGCTAGTCTATCAGCATCTGACAGTGAATTTGGATGTTCTCAGAACCATTTCA 298  
 DB 2713 AGAGCTAGTCTATCAGCATCTGACAGTGAATTTGGATGTTCTCAGAACCATTTCA 2772  
 QY 299 GACAGCTGTTTCTATCCTCTTCTTAAATAAATTTAGTTGGTCTCTACATGCATAA 358  
 DB 2773 GACAGCTGTTTCTATCCTCTTCTTAAATAAATTTAGTTGGTCTCTACATGCATAA 2832  
 QY 359 CCTGCTCCAATCTGTCACATAAAGTCTGTGACTTTGAAGTTTGTAGTACAGACCC 418  
 DB 2833 CCTGCTCCAATCTGTCACATAAAGTCTGTGACTTTGAAGTTTGTAGTACAGACCC 2892  
 QY 419 ACTTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATAAAGTACCCATG 478  
 DB 2893 ACTTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATAAAGTACCCATG 2952  
 QY 479 TCTTTA 484  
 DB 2953 TCTTTA 2958

Search completed: September 13, 2003, 02:00:53  
 Job time : 227 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 13, 2003, 00:51:46 ; Search time 1646 Seconds  
(without alignments)  
7146.638 Million cell updates/sec

Title: US-09-352-616A-434

Perfect score: 484

Sequence: 1 ttttaataaagcatttagt.....ataaagtaacctgttttta 484

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gssl:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
c 1	484	100.0	538	9	AI620178
c 2	484	100.0	663	12	BQ018482
c 3	483	99.8	661	12	BQ020946
c 4	473	97.7	599	9	AA813266

#### ALIGNMENTS

RESULT 1  
AI620178/c

LOCUS

DEFINITION

tu54a11.x1 NCI\_CGAP\_Pr28 Homo sapiens

AI620178

AI620178.1

AI620178.1

AI620178.1

AI620178.1

AI620178.1

AI620178.1

AI620178.1

AI620178.1

AI620178.1

AI620178.1

AI620178.1

AI620178.1

AI620178.1

AI620178.1

AI620178.1

AI620178.1

AI620178.1

AI620178.1

AI620178.1

AI620178.1

AI620178.1

AI620178.1

AI620178.1

AI620178.1

AI620178.1

c 5	473	97.7	674	12	BM983868
c 6	472	97.5	631	14	CA430903
c 7	469	96.9	490	9	AA437224
c 8	447	92.4	455	9	AA972883
c 9	434	89.7	434	9	AI989281
c 10	431.4	89.1	435	9	AA809587
c 11	422	87.2	423	9	AI685682
c 12	389	80.4	607	12	BI855676
c 13	386.6	79.9	419	9	AA229495
c 14	382.8	79.1	411	9	AA640928
c 15	379	78.3	383	9	AI672753
c 16	374.2	77.3	445	9	AA533772
c 17	372	76.9	423	9	AA531606
c 18	361	74.6	377	9	AI669511
c 19	360	74.4	374	14	W47380
c 20	359	74.2	366	9	AI424280
c 21	358	74.0	386	9	AI027196
c 22	356	73.6	356	9	AA507804
c 23	356	73.6	382	9	AW135064
c 24	356	73.6	391	10	BF511129
c 25	352	72.7	380	9	AA833543
c 26	348.4	72.0	371	9	AA758204
c 27	344.4	71.2	382	9	AI692186
c 28	343.2	70.9	353	9	AA508806
c 29	332.8	68.8	354	9	AA603372
c 30	330.2	68.2	337	9	AI748915
c 31	328.8	67.9	337	9	AA400418
c 32	327	67.6	403	9	AA493522
c 33	323.2	66.8	339	9	AA650104
c 34	313.4	64.8	340	9	AW006550
c 35	304	62.8	342	9	AA228941
c 36	284.2	58.7	331	10	BF095382
c 37	278.2	57.5	311	9	AA527743
c 38	276.8	57.2	361	9	AI829793
c 39	264	54.5	472	9	AA640241
c 40	262.6	54.3	282	9	AA654919
c 41	262.4	54.2	332	10	BF508160
c 42	252	52.1	283	9	AA652376
c 43	246.6	51.0	261	9	AA650230
c 44	239	49.4	267	9	AA572913
c 45	218.6	45.2	396	12	BI360784

AI620178 538 bp mRNA linear EST 15-DEC-1999  
tu54a11.x1 NCI\_CGAP\_Pr28 Homo sapiens cDNA clone IMAGE:225484 3',  
mRNA sequence.

AI620178 GI:4629304  
AI620178.1  
EST.  
Homo sapiens (human)

Keywords: Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 538)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapsb-re@mail.nih.gov](mailto:cgapsb-re@mail.nih.gov)

Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Sequencing by: Greg Lennon, Ph.D.

Clone Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Insert Length: 825 Std Error: 0.00  
Seq primer: -400P from Gibco  
High quality sequence stop: 456  
POLYA=No.

FEATURES  
source  
1. 538  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:225484"  
/sex="male"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="NCL\_CGAP\_P28"  
/note="Organ: prostate; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI-CGAP P-22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 190 a 84 c 113 g 151 t

Query Match 100.0%; Score 484; DB 9; Length 538;  
Best Local Similarity 100.0%; Pred. No. 2.6e-90;  
Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTAAATAGCAATTTAGTGCCTCAGTCCCTACTGAGTACTCTTCTCTCCCTCTCTG 60  
Db TTTTAAATAGCAATTTAGTGCCTCAGTCCCTACTGAGTACTCTTCTCTCCCTCTCTG 60

QY 61 AATTAAATCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATATATG 120  
Db AATTAAATCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATATATG 120

QY 121 TGTGCAAAAAAAGAGTGTCTTTGTTTAAATTAATTTGTTTGAATCCATCTGTC 180  
Db TGTGCAAAAAAAGAGTGTCTTTGTTTAAATTAATTTGTTTGAATCCATCTGTC 180

QY 181 TTTTCCCATGGAATAGTCTTAAATTAATTTAGTTGGGTTCTCTACATGCATAAACC 130  
Db TTTTCCCATGGAATAGTCTTAAATTAATTTAGTTGGGTTCTCTACATGCATAAACC 130

QY 129 TGCTCAATCTGCATATAAAGTCTGTGACTTGAAGTTTGAAGTTCAGCAGCCCAAC 420  
Db TGCTCAATCTGCATATAAAGTCTGTGACTTGAAGTTTGAAGTTCAGCAGCCCAAC 420

QY 421 TTTATTTTCTATGTTTGTTCACATATGAGTGTGTTGAAATTAAGTACCCATGTC 480  
Db TTTATTTTCTATGTTTGTTCACATATGAGTGTGTTGAAATTAAGTACCCATGTC 480

QY 481 TTTA 484  
Db TTTA 6

RESULT 2  
BQ018482/c  
LOCUS  
DEFINITION  
UI-H-DHI-axj-1-02-0-01.s1 NCI\_CGAP\_DHI Homo sapiens CDNA clone  
IMAGE:5829649 3', mRNA sequence.  
ACCESSION  
BQ018482

VERSION BQ018482.1 GI:19753759  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS 1 (bases 1 to 663)  
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Dr. Jose Mercuende  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
The following repetitive elements were found in this cDNA  
sequence: 1-30, >AT-rich#Low\_complexity (matched complement)  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
source  
Location/Qualifiers  
1. 663  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5829649"  
/tissue\_type="Metastatic Chondrosarcoma"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI\_CGAP\_DHI"  
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: Ecor I; Site 2: Not I; NCI-CGAP\_DHI is a normalized cDNA library containing the following tissue(s): VS-8 Cell line from Metastatic Chondrosarcoma in Lung. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGATCATTTGC.  
TAG\_LIB=UI-H-DHI  
TAG\_ISSUE=Lung  
TAG\_SEQ=AGATCATTTGC"

BASE COUNT 219 a 106 c 140 g 197 t 1 others

ORIGIN

Query Match 100.0%; Score 484; DB 12; Length 663;  
Best Local Similarity 100.0%; Pred. No. 2.5e-90;  
Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTAAATAGCAATTTAGTGCCTCAGTCCCTACTGAGTACTCTTCTCTCCCTCTCTG 60  
Db TTTTAAATAGCAATTTAGTGCCTCAGTCCCTACTGAGTACTCTTCTCTCCCTCTCTG 60

QY 61 AATTAAATCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATATATG 120  
Db AATTAAATCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATATATG 120

QY 121 TGTGCAAAAAAAGAGTGTCTTTGTTTAAATTAATTTGTTTGAATCCATCTGTC 180  
Db TGTGCAAAAAAAGAGTGTCTTTGTTTAAATTAATTTGTTTGAATCCATCTGTC 180

QY 181 TTTTCCCATGGAATAGTCTTAAATTAATTTAGTTGGGTTCTCTACATGCATAAACC 331  
Db TTTTCCCATGGAATAGTCTTAAATTAATTTAGTTGGGTTCTCTACATGCATAAACC 331

QY 330 TTTTCCCATGGAATAGTCTTAAATTAATTTAGTTGGGTTCTCTACATGCATAAACC 271  
Db TTTTCCCATGGAATAGTCTTAAATTAATTTAGTTGGGTTCTCTACATGCATAAACC 271

```
QY 241 AGCTAGTCTATCAGCATCTGACAGGTGAATGGATGGTTCTCAGAACCAATTTACCCCGAGA 300
|||||
Db 270 AGCTAGTCTATCAGCATCTGACAGGTGAATGGATGGTTCTCAGAACCAATTTACCCCGAGA 211
|||||
QY 301 CAGCCTGTTCTATCCTCTTTAAATAAATAGTTTGGGTTCTCTACATGCATAACAAACCC 360
|||||
Db 210 CAGCCTGTTCTATCCTCTTTAAATAAATAGTTTGGGTTCTCTACATGCATAACAAACCC 151
|||||
QY 361 TGCCTCAATCTGTACATATAAAGTCTGTGACTTGAAGTTTGAAGTTCAGTCAGCAGCCGCCACCAAC 420
|||||
Db 150 TGCCTCAATCTGTACATATAAAGTCTGTGACTTGAAGTTTGAAGTTCAGTCAGCAGCCGCCACCAAC 91
|||||
QY 421 TTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATAAAGTACCATGTC 480
|||||
Db 90 TTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATAAAGTACCATGTC 31
|||||
QY 481 TTTA 484
|||||
Db 30 TTTA 27

RESULT 3
BQ020946/c
LOCUS BQ020946 661 bp mRNA linear EST 27-MAR-2002
DEFINITION UI-H-DHI-axh-j-06-0-UI.s1 NCI_CGAP_DHI Homo sapiens cDNA clone
IMAGE:5828837 3', mRNA sequence.
ACCESSION BQ020946
VERSION BQ020946.1 GI:19756232
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 661)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
The following repetitive elements were found in this cDNA
sequence: 1-30, >AT-rich#Low_complexity (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
1. 661
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5828837"
/tissue_type="Metastatic Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DHI0B (Life Technologies)"
/clone_lib="NCI_CGAP_DHI"
/note="Organ: Lung; Vector: p7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_DHI is a normalized cDNA library containing the
following tissue(s): VS-8 Cell line from Metastatic
Chondrosarcoma in Lung. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into p7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
```

```
sequence tag for this library is AGATCATTTGC.
TAG_LIB=UI-H-DHI
TAG_TISSUE=lung
TAG_SEQ=AGATCATTTGC"
BASE COUNT 220 a 106 c 139 g 194 t 2 others
ORIGIN
Query Match 99.8%; Score 483; DB 12; Length 661;
Best Local Similarity 99.8%; Pred. No. 4e-90;
Matches 483; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TTTTAAATAAGCATTTAGTCTCAGTCCCTACTGAGTACACTTCTCTCCCTCCTCTG 60
|||||
Db 510 TTTTAAATAAGCATTTAGTCTCAGTCCCTACTGAGTACACTTCTCTCCCTCCTCTG 451
|||||
QY 61 AATTTAATTTCTTCAACTTGCAAATTTGCAAGATTACACATTTCACTCTGATGTATTTG 120
|||||
Db 450 AATTTAATTTCTTCAACTTGCAAATTTGCAAGATTACACATTTCACTCTGATGTATTTG 391
|||||
QY 121 TGTTCGCAAAAAAAGTGTCTTTGTTTAAAAATTAATTTGTTGTGAATCCATCTTC 180
|||||
Db 390 TGTTCGCAAAAAAAGTGTCTTTGTTTAAAAATTAATTTGTTGTGAATCCATCTTC 331
|||||
QY 181 TTTTCCCATTTGGAAGTACATTAACCCATCTCTGAAGTGTGTAGAGAAAACATCTGAAG 240
|||||
Db 330 TTTTCCCATTTGGAAGTACATTAACCCATCTCTGAAGTGTGTAGAGAAAACATCTGAAG 271
|||||
QY 241 AGCTAGTCTATCAGCATCTGACAGGTGAATGGATGGTTCTCAGAACCAATTTACCCCGAGA 300
|||||
Db 270 AGCTAGTCTATCAGCATCTGACAGGTGAATGGATGGTTCTCAGAACCAATTTACCCCGAGA 211
|||||
QY 301 CAGCCTGTTCTATCCTCTTTAAATAAATAGTTTGGGTTCTCTACATGCATAACAAACCC 360
|||||
Db 210 CAGCCTGTTCTATCCTCTTTAAATAAATAGTTTGGGTTCTCTACATGCATAACAAACCC 151
|||||
QY 361 TGCCTCAATCTGTACATATAAAGTCTGTGACTTGAAGTTTGAAGTTCAGTCAGCAGCCGCCACCAAC 420
|||||
Db 150 TGCCTCAATCTGTACATATAAAGTCTGTGACTTGAAGTTTGAAGTTCAGTCAGCAGCCGCCACCAAC 91
|||||
QY 421 TTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATAAAGTACCATGTC 480
|||||
Db 90 TTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATAAAGTACCATGTC 31
|||||
QY 481 TTTA 484
|||||
Db 30 TTTA 27

RESULT 4
AA813266/c
LOCUS AA813266 599 bp mRNA linear EST 31-DEC-1998
DEFINITION aj44903.s1 Soares_testis_NHT Homo sapiens cDNA clone 1393204 3',
mRNA sequence.
ACCESSION AA813266
VERSION AA813266.1 GI:2883251
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 599)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
```

www-bio.llnl.gov/bbrp/image/image.html  
 Insert length: 982 Std Error: 0.00  
 Seq primer: -40ml3 fwd. Err from Amersham  
 High quality sequence stop: 503.  
 Location/Qualifiers

## FEATURES

source  
 1..599  
 /organism="Homo sapiens"  
 /mol\_type="mrna"  
 /db\_xref="taxon:9606"  
 /clone="1393204"  
 /sex="male"  
 /lab\_host="DH10B"  
 /clone\_lib="Soares\_testis\_NHT"  
 /note="Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5]. TGTACCAATCTGAAGTGGAGCGCGCCCAATTTTTTTTTTTT 3]. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo."  
 202 a 98 c 131 g 168 t

BASE COUNT  
 ORIGIN

Query Match 97.7%; Score 473; DB 9; Length 599;  
 Best Local Similarity 99.8%; Pred. No. 4.9e-88;  
 Matches 484; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 TTTTAAATAAGCATTAGTGTCTAGTCCCTACTGAGTACTCTTCTCCCTCCTCTG 60  
 Db TTTTAAATAAGCATTAGTGTCTAGTCCCTACTGAGTACTCTTCTCCCTCCTCTG 434  
 QY 61 AATTAAATCTTCAACTTCCATTTGCAAGGATTACACATTTCACTGTGATGATATG 120  
 Db TTTTAAATCTTCAACTTCCATTTGCAAGGATTACACATTTCACTGTGATGATATG 374  
 QY 121 TGTTCG-AAAAAAGAGTCTTTGTTTAAATTTACTTGTGTTGTAATCCATCTG 179  
 Db TGTTCGAAAAAAGAGTCTTTGTTTAAATTTACTTGTGTTGTAATCCATCTG 314  
 QY 180 CTTTTCCTCCATGGAACATGATTAACCCATCTCTGAACCTGGTAGAAAAACATCTGAA 239  
 Db CTTTTCCTCCATGGAACATGATTAACCCATCTCTGAACCTGGTAGAAAAACATCTGAA 254  
 QY 240 GAGCTAGTCTATCAGCATCTGACAGTGAATGGATGTTCTCAGAACCATTTACCCAG 299  
 Db GAGCTAGTCTATCAGCATCTGACAGTGAATGGATGTTCTCAGAACCATTTACCCAG 194  
 QY 300 ACAGCCTGTTCTATCTCTGTTTAAATTAAGTTTGGTTCCTACATGCATAACAAACC 359  
 Db ACAGCCTGTTCTATCTCTGTTTAAATTAAGTTTGGTTCCTACATGCATAACAAACC 134  
 QY 360 CTGCTCCAATCTGCACATAAAGTCTGACTTGAAGTTAGTCAGCAGCCCAACCAAAA 419  
 Db CTGCTCCAATCTGCACATAAAGTCTGACTTGAAGTTAGTCAGCAGCCCAACCAAAA 74  
 QY 420 CTTTATTTCTATGCTGTTTTTGCACATATGAGTGTGTTTGAATAAAGTACCCATGT 479  
 Db CTTTATTTCTATGCTGTTTTTGCACATATGAGTGTGTTTGAATAAAGTACCCATGT 14  
 QY 480 CTTTA 484  
 Db TTTT 13 CTTTA 9

RESULT 5  
 BM983668/c  
 LOCUS  
 DEFINITION  
 UI-CF-DUI1-aaw-b-04-0-UI.s1 UI-CF-DUI1 Homo sapiens cDNA clone  
 674 bp mRNA linear EST 20-FEB-2003  
 UI-CF-DUI1-aaw-b-04-0-UI 3', mRNA sequence.  
 BM983668  
 ACCESSION

VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE  
 TITLES  
 AUTHORS  
 JOURNAL  
 MEDLINE  
 PUBMED  
 COMMENT

BM983668.1 GI:19608810  
 EST.  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 674)  
 Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 Genome Res. 6 (9), 791-806 (1996)  
 97044477  
 8889548  
 Contact: McCray, PB  
 McCray Lab  
 University of Iowa  
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
 Tel: 319 356 4866  
 Fax: 319 356 7171  
 Email: paul-mccray@uiowa.edu  
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.resgen.com) or from Open Biosystems  
 (www.openbiosystems.com).  
 The following repetitive elements were found in this cDNA  
 sequence: 1-21, >AT-rich#Low\_complexity (matched complement)  
 seq primer: M13 FORWARD  
 POLYA=Yes.

FEATURES  
 source

Location/Qualifiers  
 1..674  
 /organism="Homo sapiens"  
 /mol\_type="mrna"  
 /db\_xref="taxon:9606"  
 /clone="UI-CF-DUI1-aaw-b-04-0-UI"  
 /tissue\_type="Primary Lung Epithelial Cells"  
 /dev\_stage="Adult"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /clone\_lib="UI-CF-DUI1"  
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-CF-DUI1 is a normalized cDNA library containing the following tissue(s): Primary Lung Epithelial Cells The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GCCTGTAGGC.  
 TAG\_LIB=UI-CF-DUI1  
 TAG\_TISSUE=Lung Epithelial Cells Tissue nos 359-368  
 TAG\_SEQ=GGCTGTAGGC"

BASE COUNT  
 ORIGIN

221 a 111 c 144 g 198 t

Query Match 97.7%; Score 473; DB 12; Length 674;  
 Best Local Similarity 99.8%; Pred. No. 4.8e-88;  
 Matches 484; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 TTTTAAATAAGCATTAGTGTCTAGTCCCTACTGAGTACTCTTCTCCCTCCTCTG 60  
 Db TTTTAAATAAGCATTAGTGTCTAGTCCCTACTGAGTACTCTTCTCCCTCCTCTG 443  
 QY 61 AATTAAATCTTCAACTTGCATTTGCAAGATTACACATTTCACTGTGATGATATG 120  
 Db AATTAAATCTTCAACTTGCATTTGCAAGATTACACATTTCACTGTGATGATATG 383

Qy 121 TGTTCACAAAAAAGAGTCTTTGTTTAAATTAATCTGGTTGTGAATCCATCTTGC 180  
 Db 382 TGTTCACAAAAAAGAGTCTTTGTTTAAATTAATCTGGTTGTGAATCCATCTTGC 323  
 Qy 181 TTTTCCCATTCGAACTAGTCATTAACCCATCTCTGAACCTGGTAGAAAAACATCTGAAG 240  
 Db 322 TTTTCCCATTCGAACTAGTCATTAACCCATCTCTGAACCTGGTAGAAAAACATCTGAAG 263  
 Qy 241 AGCTAGTCTATCAGCATCTGACAGGTGAATGGATGTTCTCTCAGAACCATTTCCACCCAGA 300  
 Db 262 AGCTAGTCTATCAGCATCTGACAGGTGAATGGATGTTCTCTCAGAACCATTTCCACCCAGA 203  
 Qy 301 CAGCCTGTTCTATCTCCTGTTTATAAATAGTTGGGTTCTCTACATGATCAATAACAACCC 360  
 Db 202 CAGCCTGTTCTATCTCCTGTTTATAAATAGTTGGGTTCTCTACATGATCAATAACAACCC 143  
 Qy 361 TGTCCCAATCTGTCACATAAAGTCTGACTTCAAGTCTTAGTCAAGCAGCAGCCCA-CCAAA 419  
 Db 142 TGTCCCAATCTGTCACATAAAGTCTGACTTCAAGTCTTAGTCAAGCAGCAGCCCA-CCAAA 83  
 Qy 420 CTTTATTTTCTATGTTGTTTTCGCAACATATGAGTGTGTTTGAATAAAGTACCCATGT 479  
 Db 82 CTTTATTTTCTATGTTGTTTTCGCAACATATGAGTGTGTTTGAATAAAGTACCCATGT 23  
 Qy 480 CTTTA 484  
 Db 22 CTTTA 18

## RESULT 6

## CA430903/c

LOCUS CA430903 631 bp mRNA linear EST 07-NOV-2002  
 DEFINITION UI-H-FL1-bge-i-17-0-UI.s1 NCI CGAP FL1 Homo sapiens cDNA clone  
 UI-H-FL1-bge-i-17-0-UI 3', mRNA sequence.  
 ACCESSION CA430903  
 VERSION CA430903.1 GI:24793629  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 631)  
 REFERENCE NCI CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs@mail.nih.gov](mailto:cgapbs@mail.nih.gov)  
 Tissue Procurement: James Martin  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Dr. M. Bento Soares, University of Iowa  
 from Dr. M. Bento Soares, bento-soares@uiowa.edu  
 Seq primer: M13 FORWARD  
 POLYA=Yes.

## FEATURES

## source

## Location/Qualifiers

1. 631  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-H-FL1-bge-i-17-0-UI"  
 /tissue\_type="Cell lines"  
 /dev\_stage="Adult"  
 /lab\_host="DH10B (Life Technologies)"  
 /clone\_lib="NCI CGAP FL1"

/note="Organ: Chondrosarcoma; Vector: pT73-Pac (Pharmacia)  
 ) with a modified polylinker; Site:1; Ecor I; Site 2: Not  
 I; NCI CGAP FL1 is a normalized cDNA library derived from  
 a pool of mRNA obtained from 4 cell lines from grade III  
 chondrosarcoma tissues. The library was constructed  
 according to Bonaldi, Lennon and Soares, Genome Research,  
 6:791-806, 1996. First strand cDNA synthesis was primed

with an oligo-dT primer containing a Not I site. Double  
 stranded cDNA was ligated to an Ecor I adaptor, digested  
 with Not I, and cloned directionally into pT73-Pac  
 vector. The oligonucleotide used to prime the synthesis of  
 first-strand cDNA contains a library tag sequence that is  
 located between the Not I site and the (dT)18 tail. The  
 sequence tag for this library is GAGTCGGTG. The cell  
 lines were provided by Dr. James Martin from the  
 University of Iowa.

TAG LIB=UI-H-FL1

TAG\_TISSUE=Human Chondrosarcoma Grade 3 cell line mix

TAG\_SEQ=GAGTCGGTG

BASE COUNT 210 a 102 c 136 g 182 t 1 others

Query Match 97.5%; Score 472; DB 14; Length 631;

Best Local Similarity 99.8%; Pred. No. 7.8e-88;

Matches 483; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 TTTTAAATAAGCATTTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCCTCTG 60

Db 505 TTTTAAATAAGCATTTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCCTCTG 446

Qy 61 AATTAAATCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATGATATTG 120

Db 445 AA-TTAATCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATGATATTG 387

Qy 121 TGTTCACAAAAAAGAGTCTTTGTTTAAATTAATCTGGTTGTGAATCCATCTTGC 180

Db 386 TGTTCACAAAAAAGAGTCTTTGTTTAAATTAATCTGGTTGTGAATCCATCTTGC 327

Qy 181 TTTTCCCATTCGAACTAGTCATTAACCCATCTCTGAACCTGGTAGAAAAACATCTGAAG 240

Db 326 TTTTCCCATTCGAACTAGTCATTAACCCATCTCTGAACCTGGTAGAAAAACATCTGAAG 267

Qy 241 AGCTAGTCTATCAGCATCTGACAGGTGAATGGATGTTCTCAGAACCATTTCCACCCAGA 300

Db 266 AGCTAGTCTATCAGCATCTGACAGGTGAATGGATGTTCTCAGAACCATTTCCACCCAGA 207

Qy 301 CAGCCTGTTCTATCTCCTGTTTATAAATAGTTGGGTTCTCTACATGATCAATAACAACCC 360

Db 206 CAGCCTGTTCTATCTCCTGTTTATAAATAGTTGGGTTCTCTACATGATCAATAACAACCC 147

Qy 361 TGTCCCAATCTGTCACATAAAGTCTGACTTGAAGTTTGTAGTCAGCAGCCCAACCAAC 420

Db 146 TGTCCCAATCTGTCACATAAAGTCTGACTTGAAGTTTGTAGTCAGCAGCCCAACCAAC 87

Qy 421 TTTATTTTCTATCTGTTTTCGCAACATATGAGTGTGTTTGAATAAAGTACCCATGTC 480

Db 86 TTTATTTTCTATCTGTTTTCGCAACATATGAGTGTGTTTGAATAAAGTACCCATGTC 27

Qy 481 TTTTA 484

Db 26 TTTTA 23

## RESULT 7

## AA437224/c

LOCUS AA437224 490 bp mRNA linear EST 30-MAY-1997  
 DEFINITION zV54b10.s1 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE:757435  
 3' similar to contains Alu repetitive element; mRNA sequence.

## ACCESSION

AA437224

## VERSION

AA437224.1 GI:2142138

## KEYWORDS

EST

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

## REFERENCE

1 (bases 1 to 490)

## AUTHORS

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Scheinberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Willson, R.





```
QY 338 TTCTCTACATGATACAAACCCCTGCTCCAAATCTGTCCATATAAAAGTCTGTGACTTGAAG 397
|||||
Db 155 TTCTCTACATGATACAAACCCCTGCTCCAAATCTGTCCATATAAAAGTCTGTGACTTGAAG 96
|||||
QY 398 TTGTAGTCAGACACCCACCAAACTTTATTTTCTATGTGTTTGTGCAACATATGAGTGT 457
|||||
Db 95 TTGTAGTCAGACACCCACCAAACTTTATTTTCTATGTGTTTGTGCAACATATGAGTGT 36
|||||
QY 458 TTTGAAATAAAGTACCATGCTTTTA 484
|||||
Db 35 TTTGAAATAAAGTACCATGCTTTTA 9
|||||

RESULT 9
AI989281 434 bp mRNA linear EST 02-SEP-2001
LOCUS 10 prostate cancer cell line LNCap Homo sapiens cDNA, mRNA
DEFINITION
ACCESSION AI989281
VERSION AI989281.1 GI:15421029
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 434)
AUTHORS Zhang, J.S. and Smith, D.I.
TITLE High throughput screening for androgen regulated genes in LNCap
cells: identification of Hsp-2 as an androgen regulated gene over
expressed in prostate adenocarcinoma
JOURNAL Unpublished
COMMENT Contact: Zhang, Jin-San
Dept. Pathology and Lab Medicine
Mayo Clinic Cancer Center
200 1st St. SW, Rochester MN 55905, USA
Tel: 507-2660311
Fax: 507-2665193
Email: zhang.jinsan@mayo.edu.

FEATURES
Location/Qualifiers
source 1..434
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="LNCap"
/clone_lib="prostate cancer cell line LNCap"
/notes="prostate cancer metastasized to lymph node;
subtracted cDNA libraries from prostate cancer cell line
LNCap treated with androgen."
BASE COUNT 123 a 91 c 66 g 154 t
ORIGIN

Query Match 89.7%; Score 434; DB 9; Length 434;
Best Local Similarity 100.0%; Pred. No. 6.3e-80;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 CTCTTTCTCCCTCTCTGAAATTAATTTCAACTTGCATTTGCAAGGATTACAC 99
|||||
Db 1 CTCTTTCTCCCTCTCTGAAATTAATTTCAACTTGCATTTGCAAGGATTACAC 60
|||||
QY 100 ATTTCACTGTGATGATATGTTGTGCAAAAAAAGTGTCTTTGTTTAAATTAAT 159
|||||
Db 61 ATTTCACTGTGATGATATGTTGTGCAAAAAAAGTGTCTTTGTTTAAATTAAT 120
|||||
QY 160 TGCTTTGTGAATCCATCTTCTTTTCCCATTTGGAACCTAGTCAATTAACCCATCTCGAA 219
|||||
Db 121 TGGTTGTGAATCCATCTTCTTTTCCCATTTGGAACCTAGTCAATTAACCCATCTCGAA 180
|||||
QY 220 CTGGTAGAAAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGGTT 279
|||||
Db 181 CTGGTAGAAAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGGTT 240
|||||
QY 280 CTCAGAACCAATTTTACCACAGACAGCCTGTTTCTATCTCTGTTTAAATAAATTAGTTGGTT 339
|||||

Db 241 CTCAGAACCAATTTTACCACAGACAGCCTGTTTCTATCTCTGTTTAAATAAATTAGTTGGTT 300
|||||
QY 340 CTCTACATGATACAAACCCCTGCTCCAAATCTGTCCATATAAAAGTCTGTGACTTGAAGTT 399
|||||
Db 301 CTCTACATGATACAAACCCCTGCTCCAAATCTGTCCATATAAAAGTCTGTGACTTGAAGTT 360
|||||
QY 400 TAGTCAGACACCCACCAAACTTTATTTTCTATGTGTTTGTGCAACATATGAGTGTGT 459
|||||
Db 361 TAGTCAGACACCCACCAAACTTTATTTTCTATGTGTTTGTGCAACATATGAGTGTGT 420
|||||
QY 460 TGAATAAAGTAC 473
|||||
Db 421 TGAATAAAGTAC 434
|||||

RESULT 10
AA809587 435 bp mRNA linear EST 18-FEB-1998
LOCUS n743ell.s1 NCI_CGAP_Pr9 Homo sapiens cDNA clone IMAGE:995276, mRNA
DEFINITION
ACCESSION AA809587
VERSION AA809587.1 GI:2878993
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 435)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/hc/cgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo F. Chuaqui,
M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 605 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham.

FEATURES
Location/Qualifiers
source 1..435
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:995276"
/sex="male"
/tissue_type="normal prostatic epithelial cells"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Pr9"
/notes="Organ: prostate; Vector: pAMP10; mRNA made from
normal prostatic epithelial cells, cDNA made by oligo-dT
priming. Non-directionally cloned. Size-selected on
agarose gel, average insert size 600 bp. Library made by
D. Krizman, NIH."
BASE COUNT 120 a 96 c 68 g 151 t
ORIGIN

Query Match 89.1%; Score 431.4; DB 9; Length 435;
Best Local Similarity 99.8%; Pred. No. 2.2e-79;
Matches 432; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 22 CTAGTCCCCTACTGAGTACTCTTCTCTCCCTCTCTGAATTTAAATTTCAACTTGC 81
|||||
Db 3 CTAGTCCCCTACTGAGTACTCTTCTCTCCCTCTCTGAATTTAAATTTCAACTTGC 62
|||||
QY 82 AATTTGCAAGGATTACACATTTCACTGTGATATATTTGTTGCAAAAAAAGT 141
|||||
```

Db 63 AATTTCAGCAATACACATTTCACTGTGATGTATATGTGTGCAAAAAAAGTG 122

QY 142 TCTTTGTTAAATTAATCTGTTGTGAATCCATCTTGTCTTCCCATTTGGAACAGT 201

Db 123 TCTTTGTTAAATTAATCTGTTGTGAATCCATCTTGTCTTCCCATTTGGAACAGT 182

QY 202 CATTAAACCCATCTGTAACCTGGTAGAATAACATCTGAAGAGCTAGTCTATFAGCATCTGA 261

Db 183 CATTAAACCCATCTGTAACCTGGTAGAATAACATCTGAAGAGCTAGTCTATFAGCATCTGA 242

QY 262 CAGTGAATTTGGATGTTCTCAGAACCATTTACCCAGACAGCTGTTCTATCCGTTT 321

Db 243 CAGTGAATTTGGATGTTCTCAGAACCATTTACCCAGACAGCTGTTCTATCCGTTT 302

QY 322 AATAAATAGTTTGGTGTCTACATGCATAAACAACCTGCTCCAACTGTGCACATAAA 381

Db 303 AATAAATAGTTTGGTGTCTACATGCATAAACAACCTGCTCCAACTGTGCACATAAA 362

QY 382 AGTCTGTGACTTCAAGTTTAGTCAGACCCACCAACCACTTTATTTTCTATGTGTTTT 441

Db 363 AGTCTGTGACTTCAAGTTTAGTCAGACCCACCAACCACTTTATTTTCTATGTGTTTT 422

QY 442 TGAACATATGAG 454

Db 423 TGAACATATGAG 435

RESULT 11

AI685682/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AI685682

423 bp mRNA linear EST 27-MAY-1999

tt89h03.x1 NCI\_CGAP\_Pr28 Homo sapiens CDNA clone IMAGE:2248757 3',

mRNA sequence.

AI685682.1 GI:4896976

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Seq primer: -400P from Gibco.

Location/Qualifiers

1. 423

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2248757"

/sex="male"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="NCI\_CGAP\_Pr28"

/note="Organ: prostate; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI\_CGAP\_Pr22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonids 985608-986759, 1101192-1101959, and 1217928-1220615).

BASE COUNT

150 a 66 c 83 g 124 t

ORIGIN

Query Match

Best Local Similarity 87.2%; Score 422; DB 9; Length 423;

Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 TTTAATCTTTCAACTTGCAGGATTCACATTTCACTGTGATGTATATGTG 122

Db 423 TTTAATCTTTCAACTTGCAGGATTCACATTTCACTGTGATGTATATGTG 364

QY 123 TTGCAAAAAAAGAGTCTTCTTTAAATTAATCTTGGTTGTGAATCCATCTTGTCTT 182

Db 363 TTGCAAAAAAAGAGTCTTCTTTAAATTAATCTTGGTTGTGAATCCATCTTGTCTT 304

QY 183 TTTCCTCCATTTGGAATAGTCAATTAACCATCTCTGAAGTGTAGAAAAACATCTGAAG 242

Db 303 TTTCCTCCATTTGGAATAGTCAATTAACCATCTCTGAAGTGTAGAAAAACATCTGAAG 244

QY 243 CTAGTCTATCAGCATCTCAGAGTGAATTTGGATGTTCTCAGAACCATTTCCACCCAGACA 302

Db 243 CTAGTCTATCAGCATCTCAGAGTGAATTTGGATGTTCTCAGAACCATTTCCACCCAGACA 184

QY 303 GCCTGTTTCTATCTCTGTTTAATAAATAGTTTGGGTTCTCTACATGCATACAAACCTG 362

Db 183 GCCTGTTTCTATCTCTGTTTAATAAATAGTTTGGGTTCTCTACATGCATACAAACCTG 124

QY 363 CTCCAATCTGTACATATAAAGTCTGTGACTTGAAGTTTAGTCAGCAGCCCAACCAACTT 422

Db 123 CTCCAATCTGTACATATAAAGTCTGTGACTTGAAGTTTAGTCAGCAGCCCAACCAACTT 64

QY 423 TATTTTCTATGTTGTTTTCGAACATATGAGTCTTTTGAATAAAGTACCCATCTT 482

Db 63 TATTTTCTATGTTGTTTTCGAACATATGAGTCTTTTGAATAAAGTACCCATCTT 4

QY 483 TA 484

Db 3 TA 2

RESULT 12

BI855676/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BI855676

607 bp mRNA linear EST 10-OCT-2001

603383205F2 NIH\_MGC\_87 Homo sapiens CDNA clone IMAGE:5392201 5',

mRNA sequence.

BI855676

BI855676.1 GI:15996423

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: DCTD/DTF

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLAM1999 row: i column: 02

High quality sequence stop: 586.

Location/Qualifiers

1. 607

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

FEATURES

source

```
/clone="IMAGE:5392201"
/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_87"
/clone="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dr primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT      215 a      86 c      139 g      167 t
ORIGIN
```

```
Query Match      80.4%; Score 389; DB 12; Length 607;
Best Local Similarity 96.6%; Pred. No. 1.3e-70;
Matches 451; Conservative 0; Mismatches 10; Indels 6; Gaps 5;

QY 20 TGCACAGCCCTACTGAGTACTCTTCTCTCCCTCCCTCTGAATTAATTTCTTCACTT 79
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 469 TCCACAGCCCTACTGAGTACTCTTCTCTCCCTCCCTCTGAATTAATTTCTTCACTT 410
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 80 GCAATTTGCA-AGGATTACACATTTCACTGTGATGATATATTTGTGTG-CAAAAA 137
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 409 GCCATTTCACAGGATTACACATTTCACTGTGAGTATATTTGTGTGCCAAAAA 350
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 138 AGTGTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTTGTCTTTTCCCATTTGGAAC 197
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 349 AGTGTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTTGTCTTTTCCCATTTGGAAC 290
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 198 TAGTCATTAACCCATCTCTGAACCTGGTAGAAAAACATCTGAAGACTAGTCTATCAGCAT 257
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 289 TAGTCATTAACCCATCTCTGAACCTGGTAGAAAAACATCTGAAGACTAGTCTATCAGCAT 230
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 258 CTGACAGGTGAATTTGGATGGTTCTCAGAACCATTTACCCAGACAGCCCTGTTCTATCCT 317
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 229 CTGACAGGTGAATTTGGATGGTTCTCAGAACCATTTACCCAGACAGCCCTGTTCTATCCT 170
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 318 GTTTAATAAATTTAGTTGGTTTCTACATGCATAACAAACCCCTGCCATCTGTCTACA 377
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 169 GTTTAATAAATTTAGTTGGTTTCTACATGCATAACAA--CCCTGTCTCCATCTGTCTACA 112
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 378 TAAAGTCTGTGACTTGAAGTTTGTAGTACGACACCCACCAACACTTTATTTCTATGTGT 437
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 111 TAAAGTCTGTGACTTGAAGTTTGTAGTACGACACCCACCAACACTTTATTTCTATGTGT 53
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 438 TTTTGGCAACATATGAGTGTGTTTGAATAAAGTACCCATGCTCTTTA 484
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 52 TTTTGG-ACATATGAGTGTGTTTGAATAAAGTACCCATGCTCTTTA 7
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

```
RESULT 13
AA229495/c
LOCUS      AA229495      419 bp      mRNA      linear      EST 21-AUG-1997
DEFINITION nc35a03.s1 NCI_CGAP_pr2 Homo sapiens CDNA clone IMAGE:1010092
            similar to contains Alu repetitive element; mRNA sequence.
ACCESSION  AA229495
VERSION     AA229495.1 GI:1851569
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 419)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished
CONTACT     Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.
            , Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
```

```
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 856 Std Error: 0.00
Seq Primer: 41ml3 fwd. ET from Amersham
High quality sequence stop: 368.
Location/Qualifiers
1. 419
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1010092"
/sex="Male"
/dev_stage="45 years old"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Pr2"
/note="Vector: PAMPI0; Site_1: NotI; Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNase-treated, total cellular RNA obtained from 5,000-10
,000 microdissected preneoplastic cells
histologically-determined to be prostatic intraepithelial
neoplasia 2 (PIN2) cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into PAMPI0 by the UDG-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman."
BASE COUNT      141 a      68 c      79 g      131 t
ORIGIN
```

```
Query Match      79.9%; Score 386.6; DB 9; Length 419;
Best Local Similarity 98.5%; Pred. No. 4.3e-70;
Matches 401; Conservative 0; Mismatches 4; Indels 2; Gaps 1;

QY 80 GCAATTTGCAAGGATTACACATTTCACTGTGATGATATTTGTGTGC--AAAAA 137
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 419 GCAATTTGCAAGGATTACACATTTCACTGTGATGATATTTGTGTGCAAAAAA 360
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 138 AGTGTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTTGTCTTTTCCCATTTGGAAC 197
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 359 AGTGTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTTGTCTTTTCCCATTTGGAAC 300
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 198 TAGTCATTAACCCATCTCTGAACCTGGTAGAAAAACATCTGAAGACTAGTCTATCAGCAT 257
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 299 TAGTCATTAACCCATCTCTGAACCTGGTAGAAAAACATCTGAAGACTAGTCTATCAGCAT 240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 258 CTGACAGGTGAATTTGGATGGTTCTCAGAACCATTTACCCAGACAGCCCTGTTCTATCCT 317
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 239 CTGACAGGTGAATTTGGATGGTTCTCAGAACCATTTACCCAGACAGCCCTGTTCTATCCT 180
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 318 GTTTAATAAATTTAGTTGGTTTGTAGTACATGCATAACAAACCCCTGCCATCTGTCTACA 377
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 179 GTTTAATAAATTTAGTTGGTTTGTAGTACATGCATAACAAACCCCTGCCATCTGTCTACA 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 378 TAAAGTCTGTGACTTGAAGTTTGTAGTACGACACCCACCAACACTTTATTTCTATGTGT 437
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 119 TAAAGTCTGTGACTTGAAGTTTGTAGTACGACACCAACCAACACTTTATTTCTATGTGT 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 438 TTTTGGCAACATATGAGTGTGTTTGAATAAAGTACCCATGCTCTTTA 484
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 59 TTTTGGCAACATATGAGTGTGTTTGAATAAAGTACCCAGGCTCTTTA 13
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

```
RESULT 14
AA640928
LOCUS      AA640928      411 bp      mRNA      linear      EST 27-OCT-1997
DEFINITION nr28d08.r1 NCI_CGAP_Pr3 Homo sapiens CDNA clone IMAGE:1169295, mRNA
            sequence.
ACCESSION  AA640928
VERSION     AA640928.1 GI:2566178
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
```

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 411)  
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs@mail.nih.gov  
 Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.  
 , Michael Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: David B. Krizman, Ph.D.  
 DNA Sequencing by: Genome Systems Inc., Greg Lennon, Ph.D.  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
 Seq primer: -28m13 revl Et from Amersham  
 High quality sequence stop: 387.  
 FEATURES  
 Location/Qualifiers  
 1..411  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1169295"  
 /sex="Male"  
 /dev\_stage="45 years old"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI-CGAP\_Pr3"  
 /note="Vector: pAMP10; Site\_1: Not1; Site\_2: EcoRI; 1st  
 strand cDNA was primed with oligo(dT)17 on 50 ng of  
 DNase-treated, total cellular RNA obtained from 5,000-10  
 ,000 microdissected cells histologically-determined to be  
 fully malignant prostate cancer cells. Double-stranded  
 cDNA was ligated to EcoRI adaptors, 5 cycles of PCR  
 applied to the cDNA with an adaptor-specific primer, and  
 the resulting PCR product subcloned into pAMP10 by the  
 UDG-cloning method (Life Technologies). Average insert  
 size is 600 bp. NOTE: Not directionally cloned. This  
 library was constructed by David Krizman."  
 BASE COUNT 123 a 80 c 68 g 140 t  
 ORIGIN

Query Match 79.1%; Score 382.8; DB 9; Length 411;  
 Best Local Similarity 99.2%; Pred. No. 2.6e-69;  
 Matches 395; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
 QY 88 CAAGGATTACACATTTCACTGTCATGTATATTTGTTGCG-AAAAAAAAAAGTGTCTT 146  
 DB 5 CAAGGATTACACATTTCACTGTCATGTATATTTGTTGCG-AAAAAAAAAAGTGTCTT 64  
 QY 147 GTTTAAATTAAGTGTGTTGTAATCCATCTTGTCTTTTCCCATTTGGAAGTGTCTT 206  
 DB 65 GTTTAAATTAAGTGTGTTGTAATCCATCTTGTCTTTTCCCATTTGGAAGTGTCTT 124  
 QY 207 ACCCATCTCTGAACCTGGTAGAAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAGT 266  
 DB 125 ACCCATCTCTGAACCTGGTAGAAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAGT 184  
 QY 267 GAATGGATGGTTCTCAGAACCATTTACCCAGACAGCGTGTCTATCTGTTTAAATAA 326  
 DB 185 GAATGGATGGTTCTCAGAACCATTTACCCAGACAGCGTGTCTATCTGTTTAAATAA 244  
 QY 327 ATTAGTTTGGTCTCTACATGCATACAAACCCCTGCTCCAAATCTGTCATAAAAGTCT 386  
 DB 245 ATTAGTTTGGTCTCTACATGCATACAAACCCCTGCTCCAAATCTGTCATAAAAGTCT 304  
 QY 387 GTGACTTGAAGTTTAGTCAGCACCCGCCAACAACTTTATTTTCTATGTTGTTTTCGAA 446  
 DB 305 GTGACTTGAAGTTTAGTCAGCACCCGCCAACAACTTTATTTTCTATGTTGTTTTCGAA 364  
 QY 447 CATATGAGTGTGTTTGAATAAAGTAGTACCCATGCTTTTA 484

Db 365 CATATGAGTGTGTTTGAATAAAGTAGTACCCATGCTTTTA 402  
 RESULT 15  
 LOCUS AI672753  
 DEFINITION we58d10.x1 Soares thymus NHPT Homo sapiens cDNA clone  
 IMAGE:2345299 3' similar to contains Alu repetitive element.; mRNA  
 sequence.  
 ACCESSION AI672753.1 GI:4852484  
 VERSION EST.  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 383)  
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs@mail.nih.gov  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium ([infoimage.llnl.gov](http://infoimage.llnl.gov)) for further information.  
 Insert Length: 1465 Std Error: 0.00  
 Seq primer: -400P from Gibco  
 High quality sequence stop: 362.  
 FEATURES  
 Location/Qualifiers  
 1..383  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2345299"  
 /dev\_stage="fetal"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="Soares\_thymus\_NHPT"  
 /note="Organ: thymus, pooled; Vector: pT7T3D-Pac  
 (Pharmacia) with a modified polylinker; Site\_1: Not I;  
 Site\_2: Eco RI; 1st strand cDNA was primed with a Not I -  
 oligo(dT) primer [5'  
 TGTACCAATCTGAAGTGGAGCGCGCGCAAGCTTTTCTTTTCTTTTCTTTT 3']  
 double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I  
 and Eco RI sites of the modified pT7T3 vector. Library  
 went through one round of normalization. Library  
 constructed by Bento Soares and M. Fatima Bonaldo."  
 BASE COUNT 134 a 63 c 75 g 111 t  
 ORIGIN

Query Match 78.3%; Score 379; DB 9; Length 383;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-68;  
 Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 106 CTGTGATGTATATTTGTTGCAAAAAAAGTGTCTTTGTTTAAATTTACTTGT 165  
 DB 383 CTGTGATGTATATTTGTTGCAAAAAAAGTGTCTTTGTTTAAATTTACTTGT 324  
 QY 166 GTGAATCCATCTTGTCTTTTCCCATTTGGAAGTGTCTATTAACCCATCTCTGAAGT 225  
 DB 323 GTGAATCCATCTTGTCTTTTCCCATTTGGAAGTGTCTATTAACCCATCTCTGAAGT 264  
 QY 226 GAAATAACATCTGAAGAGCTAGTCTATCAGCATCTGCAGGTGAATTTGATGTTCTCAGA 285  
 DB 263 GAAATAACATCTGAAGAGCTAGTCTATCAGCATCTGCAGGTGAATTTGATGTTCTCAGA 204  
 QY 286 ACCATTTTCAACCCAGACAGCTGTTTCTATCTCTTTTAATTAATAGTTGGTGTCTAC 345  
 DB 203 ACCATTTTCAACCCAGACAGCTGTTTCTATCTCTTTTAATTAATAGTTGGTGTCTAC 144  
 QY 346 ATGCATAACAACCCCTCTCCAATCTGTGCATAAAAGTCTGTGACTTGAAGTTAGTCA 405  
 |||||||

Db 143 ATGCATTAACAACCCCTGCTCCAATCTGTCACATAAAAGTCTGTGACTTTGAAGTTTAGTCA 84  
Qy 406 GCACCCCCACCAAACTTTATTTTCTATGTGTTTTTGTGCAACATATGAGTGTGTTTGA AAA 465  
Db 83 GCACCCCCACCAAACTTTATTTTCTATGTGTTTTTGTGCAACATATGAGTGTGTTTGA AAA 24  
Qy 466 TAAAGTACCCATGCTTTTA 484  
Db 23 TAAAGTACCCATGCTTTTA 5

Search completed: September 13, 2003, 02:28:29  
Job time : 1651 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 13, 2003, 01:51:10 ; Search time 55 Seconds  
(without alignments)  
3884.172 Million cell updates/sec

Title: US-09-352-616A-434  
Perfect score: 484  
Sequence: 1 ttttaataaagcatttagt.....ataaagtaccatgtcttta 484

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA.\*

- 1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	484	100.0	484	US-09-439-313-434	Sequence 434, App
2	484	100.0	484	US-09-352-616A-434	Sequence 434, App
3	472	97.5	2051	US-09-328-475C-334	Sequence 334, App
4	472	97.5	2984	US-09-439-313-335	Sequence 335, App
5	472	97.5	2984	US-09-352-616A-335	Sequence 335, App
6	472	97.5	2984	US-09-232-149A-335	Sequence 335, App
7	426.2	88.1	1020	US-09-328-475C-102	Sequence 102, App
8	426.2	88.1	1021	US-09-328-475C-103	Sequence 103, App
9	415.6	85.9	822	US-09-328-475C-223	Sequence 223, App
10	382.8	79.1	497	US-09-328-475C-222	Sequence 222, App
11	365	75.4	366	US-09-020-956-115	Sequence 115, App
12	365	75.4	366	US-09-030-607-115	Sequence 115, App
13	365	75.4	366	US-09-439-313-115	Sequence 115, App
14	365	75.4	366	US-09-352-616A-115	Sequence 115, App
15	365	75.4	366	US-09-232-149A-115	Sequence 115, App
16	332	68.6	335	US-09-439-313-453	Sequence 453, App
17	332	68.6	335	US-09-020-956-141	Sequence 141, App
18	332	68.6	335	US-09-030-607-141	Sequence 141, App
19	332	68.6	335	US-09-439-313-141	Sequence 141, App
20	332	68.6	335	US-09-352-616A-141	Sequence 141, App
21	305.6	63.1	317	US-09-232-149A-141	Sequence 141, App
22	305.6	63.1	317	US-09-439-313-453	Sequence 453, App
23	292.6	60.5	305	US-09-352-616A-453	Sequence 453, App
24	292.6	60.5	305	US-09-439-313-295	Sequence 295, App
25	292.6	60.5	305	US-09-352-616A-295	Sequence 295, App
26	181	37.4	181	US-09-232-149A-295	Sequence 295, App
27	181	37.4	181	US-09-222-575-33	Sequence 33, App

ALIGNMENTS

RESULT 1

US-09-439-313-434  
; Sequence 434, Application US/09439313  
; Patent No. 6329505

GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan Louise

; APPLICANT: Jiang Yuqi

; APPLICANT: Reed, Steven G.

; APPLICANT: Kalos, Michael

; APPLICANT: Fanger, Gary

; APPLICANT: Retter, Mark

; APPLICANT: Solk, John

; APPLICANT: Day, Craig

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C9

; CURRENT APPLICATION NUMBER: US/09/439,313

; CURRENT FILING DATE: 1999-11-12

; NUMBER OF SEQ ID NOS: 575

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 434

; LENGTH: 484

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-439-313-434

Query Match 100.0%; Score 484; DB 4; Length 484;

Best Local Similarity 100.0%; Pred. No. 6.5e-121; Mismatches 0; Indels 0; Gaps 0;

Matches 484; Conservative 0; Indels 0; Gaps 0;

QY 1 TTTTAAATAAGCATTTAGTGTCTAGTCCCTACTGAGTACTCTTTCTCTCCCTCTCTG 60

Db 1 TTTTAAATAAGCATTTAGTGTCTAGTCCCTACTGAGTACTCTTTCTCTCCCTCTCTG 60

QY 61 AATTAAATCTTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATGATATG 120

Db 61 AATTAAATCTTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATGATATG 120

QY 121 TGTTCACAAAAAAGAGTCTTTGTTTAAATTTACTTTGGTTGTGAATCCATCTTGC 180

Db 121 TGTTCACAAAAAAGAGTCTTTGTTTAAATTTACTTTGGTTGTGAATCCATCTTGC 180

QY 181 TTTTTCCTCCATTTGGAACCTAGTCTTAACCCATCTCTGAACCTGGTAGAAAAACATCTGAAG 240

Db 181 TTTTTCCTCCATTTGGAACCTAGTCTTAACCCATCTCTGAACCTGGTAGAAAAACATCTGAAG 240

QY 241 AGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGTTCTCAGAACCATTTTACCCAGA 300

Db 241 AGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGTTCTCAGAACCATTTTACCCAGA 300

[illegible]

```

RESULT 2
US-09-352-616A-434
; Sequence 434, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocke, Susan Louise
; APPLICANT: Jiang, Yuqi
; APPLICANT: Xu, Jiaanghun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 434
; LENGTH: 484
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-352-616A-434

```

Query Match	100.0%;	Score 484;	DB 4;	Length 484;
Best Local Similarity	100.0%;	Pred. No. 6.5e-121;		
Matches 484;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	TTTTAAATTAAGCATTTAGTGCCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTG	60	
Db	1	TTTTAAATTAAGCATTTAGTGCCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTG	60	
Qy	61	AATTTAATTCCTTCAACTTGCATTTGCAAGGATTTACATTTCACTGTGATGATATTG	120	
Db	61	AATTTAATTCCTTCAACTTGCATTTGCAAGGATTTACATTTCACTGTGATGATATTG	120	
Qy	121	TGTTGCAAAAAAAGTGTCTTTGTTTAAATTTACTTGGTTGTGATCCAATCTGC	180	
Db	121	TGTTGCAAAAAAAGTGTCTTTGTTTAAATTTACTTGGTTGTGATCCAATCTGC	180	
Qy	181	TTTTTCCCATTTGGAACTAGTCATTAACCCATCTCTGAACTGGTAGAAAAACATCTGAAG	240	
Db	181	TTTTTCCCATTTGGAACTAGTCATTAACCCATCTCTGAACTGGTAGAAAAACATCTGAAG	240	
Qy	241	AGCTAGTCTATCAGCATCTGACAGTGAATTCGGATGGTTCTCAGAACCATTTTACCCAGA	300	
Db	241	AGCTAGTCTATCAGCATCTGACAGTGAATTCGGATGGTTCTCAGAACCATTTTACCCAGA	300	
Qy	301	CAGCCTGTTTCTATCCTGTTTAAATAATTAGTFTTGGGTTTCTCTACATGCATAACAAACCC	360	
Db	301	CAGCCTGTTTCTATCCTGTTTAAATAATTAGTFTTGGGTTTCTCTACATGCATAACAAACCC	360	
Qy	361	TGCTCCAATCTGCATATAAAGTCGTGACTTGAAGTTTAGTCAGCACCCCAACCAAC	420	

Db	361	TGTCCTCAATCTGTCACATAAAAGCTGTGACTTTGAAGTTT	AGTCAGCACACCCCCACCAAAAC	420
Qy	421	TTTATTTTCTATGTGTTTTTTTGCACACATATGAGTGT	TTTGAATAATAAGTACCCATGTC	480
Db	421	TTTATTTTCTATGTGTTTTTTTGCACACATATGAGTGT	TTTGAATAATAAGTACCCATGTC	480
Qy	481	TTTA	484	
Db	481	TTTA	484	

```

RESULT 3
US-09-328-475C-334/c
; Sequence 334, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 334
; LENGTH: 2051
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2051)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-334

```

Query Match	97.5%;	Score 472;	DB 4;	Length 2051;	
Best Local Similarity	99.6%;	Pred. No. 1.7e-117;			
Matches 484;	Conservative	0;	Mismatches 0;	Indels 2;	Gaps 1;
QY	1	TTTTAAATAAGCATTTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTG	60		
Db	854	TTTTAAATAGCATTTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTG	795		
QY	61	AATTTAATCTTTCAACTTTGCAAGTATTCACATTTTCACCTGTGATGTATATG	120		
Db	794	AATTTAATCTTTCAACTTTGCAAGTATTCACATTTTCACCTGTGATGTATATG	735		
QY	121	TGTTGC--AAAAAATAAAAGTGCTTTGTTTAAAAATTCATTTGTGTAATCATCTT	178		
Db	734	TGTTGCANAAAAAATAAAAGTGCTTTGTTTAAAAATTCATTTGTGTAATCATCTT	675		
QY	179	GCTTTTCCCATTTGGAAGTCTGATTAACCCATCTCTGAACTCGTAGAAAAACATCTGA	238		
Db	674	GCTTTTCCCATTTGGAAGTCTGATTAACCCATCTCTGAACTCGTAGAAAAACATCTGA	615		
QY	239	AGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGGTTCTCAGAACCATTTACCCCA	298		
Db	614	AGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGGTTCTCAGAACCATTTACCCCA	555		
QY	299	GACAGCCTGTTTCTATCCTCTGTTTAAATAAAATAGTTTGGGTGTTCTCATCATCATCAACAAC	358*		
Db	554	GACAGCCTGTTTCTATCCTCTGTTTAAATAAAATAGTTTGGGTGTTCTCATCATCAACAAC	495		
QY	359	CTGCTCCATCTCTGACATAAAGTCTGTGACTTTGAAGTTTGTAGTCAGCACCCCCACCAA	418		
Db	494	CTGCTCCATCTCTGACATAAAGTCTGTGACTTTGAAGTTTGTAGTCAGCACCCCCACCAA	435		



Qy 419 ACTTTATTTTCTATGTTGTTTTTGCAACATATAGAGTGTGTTTTGAAAAATAAGTACCCATG 478  
|||||  
Db 434 ACTTTATTTTCTATGTTGTTTTTGCAACATATAGAGTGTGTTTTGAAAAATAAGTACCCATG 375  
  
Qy 479 TCTTTA 484  
|||||  
Db 374 TCTTTA 369

RESULT 4  
US-09-439-313-335  
; Sequence 335, Application US/09439313  
; Patent No. 6329505  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan Louise  
; APPLICANT: Jiang Yuqui  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Kalos, Michael  
; APPLICANT: Fanger, Gary  
; APPLICANT: Retter, Mark  
; APPLICANT: Solk, John  
; APPLICANT: Day, Craig  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
; FILE REFERENCE: 210121.427C9  
; CURRENT APPLICATION NUMBER: US/09/439,313  
; CURRENT FILING DATE: 1999-11-12  
; NUMBER OF SEQ ID NOS: 575  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 335  
; LENGTH: 2984  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-439-313-335

Query Match 97.5%; Score 472; DB 4; Length 2984;  
Best Local Similarity 99.6%; Pred. No. 1.9e-117;  
Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;  
  
Qy 1 TTTTAAATAAGCATTTAGTGCAGTCCCTACTGAGTACTCTTTCTCCCTCCCTCTG 60  
|||||  
Db 2473 TTTTAAATAAGCATTTAGTGCAGTCCCTACTGAGTACTCTTTCTCCCTCCCTCTG 2532  
  
Qy 61 AATTTAATCTTTCAACTTGCAATTTGCAAGGATTACACATTTTCACTGTGATGATATG 120  
|||||  
Db 2533 AATTTAATCTTTCAACTTGCAATTTGCAAGGATTACACATTTTCACTGTGATGATATG 2592  
  
Qy 121 TGTGTC--AAAAAATAAGTGTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTT 178  
|||||  
Db 2593 TGTGCAAAAAATAAGTGTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTT 2652  
  
Qy 179 GCTTTTCCCATTTGGAATCTGATTAACCCATCTCTGAATCTCTGAATCTCTGAATCTCTGA 238  
|||||  
Db 2653 GCTTTTCCCATTTGGAATCTGATTAACCCATCTCTGAATCTCTGAATCTCTGAATCTCTGA 2712  
  
Qy 239 AGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGGTCTCTCAGAACCATTTTCAACCA 298  
|||||  
Db 2593 TGTGCAAAAAATAAGTGTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTT 2652  
  
Qy 179 GCTTTTCCCATTTGGAATCTGATTAACCCATCTCTGAATCTCTGAATCTCTGAATCTCTGA 238  
|||||  
Db 2653 GCTTTTCCCATTTGGAATCTGATTAACCCATCTCTGAATCTCTGAATCTCTGAATCTCTGA 2712  
  
Qy 239 AGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGGTCTCTCAGAACCATTTTCAACCA 298  
|||||  
Db 2713 AGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGGTCTCTCAGAACCATTTTCAACCA 2772  
  
Qy 299 GACAGCCTGTTTCTATCCTCTGTTTAAATTTAGTTTGGGTTCTCTACATGCATAAACAAC 358  
|||||  
Db 2773 GACAGCCTGTTTCTATCCTCTGTTTAAATTTAGTTTGGGTTCTCTACATGCATAAACAAC 2832  
  
Qy 359 CTTGCTCCAATCTGTCACATAAAGTCTGTGACTTGAAGTTTGGGTTCTCTACATGCATAAACAAC 418  
|||||  
Db 2833 CTTGCTCCAATCTGTCACATAAAGTCTGTGACTTGAAGTTTGGGTTCTCTACATGCATAAACAAC 2892  
  
Qy 419 ACTTTATTTTCTATGTTGTTTTTGCAACATATAGAGTGTGTTTTGAAAAATAAGTACCCATG 478  
|||||  
Db 2893 ACTTTATTTTCTATGTTGTTTTTGCAACATATAGAGTGTGTTTTGAAAAATAAGTACCCATG 2952

RESULT 6  
US-09-232-149A-335  
; Sequence 335, Application US/09232149A

Qy 479 TCTTTA 484  
|||||  
Db 2953 TCTTTA 2958

RESULT 5  
US-09-352-616A-335  
; Sequence 335, Application US/09352616A  
; Patent No. 6395278  
; GENERAL INFORMATION:  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Harlocker, Susan Louise  
; APPLICANT: Jiang, Yuqui  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Mitcham, Jennifer Lynn  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS  
; FILE REFERENCE: 210121.427C8  
; CURRENT APPLICATION NUMBER: US/09/352.616A  
; CURRENT FILING DATE: 1999-07-13  
; NUMBER OF SEQ ID NOS: 472  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 335  
; LENGTH: 2984  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-352-616A-335

Query Match 97.5%; Score 472; DB 4; Length 2984;  
Best Local Similarity 99.6%; Pred. No. 1.9e-117;  
Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;  
  
Qy 1 TTTTAAATAAGCATTTAGTGCAGTCCCTACTGAGTACTCTTTCTCCCTCCCTCTG 60  
|||||  
Db 2473 TTTTAAATAAGCATTTAGTGCAGTCCCTACTGAGTACTCTTTCTCCCTCCCTCTG 2532  
  
Qy 61 AATTTAATCTTTCAACTTGCAATTTGCAAGGATTACACATTTTCACTGTGATGATATG 120  
|||||  
Db 2533 AATTTAATCTTTCAACTTGCAATTTGCAAGGATTACACATTTTCACTGTGATGATATG 2592  
  
Qy 121 TGTGTC--AAAAAATAAGTGTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTT 178  
|||||  
Db 2593 TGTGCAAAAAATAAGTGTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTT 2652  
  
Qy 179 GCTTTTCCCATTTGGAATCTGATTAACCCATCTCTGAATCTCTGAATCTCTGAATCTCTGA 238  
|||||  
Db 2653 GCTTTTCCCATTTGGAATCTGATTAACCCATCTCTGAATCTCTGAATCTCTGAATCTCTGA 2712  
  
Qy 239 AGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGGTCTCTCAGAACCATTTTCAACCA 298  
|||||  
Db 2713 AGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGGTCTCTCAGAACCATTTTCAACCA 2772  
  
Qy 299 GACAGCCTGTTTCTATCCTCTGTTTAAATTTAGTTTGGGTTCTCTACATGCATAAACAAC 358  
|||||  
Db 2773 GACAGCCTGTTTCTATCCTCTGTTTAAATTTAGTTTGGGTTCTCTACATGCATAAACAAC 2832  
  
Qy 359 CTTGCTCCAATCTGTCACATAAAGTCTGTGACTTGAAGTTTGGGTTCTCTACATGCATAAACAAC 418  
|||||  
Db 2833 CTTGCTCCAATCTGTCACATAAAGTCTGTGACTTGAAGTTTGGGTTCTCTACATGCATAAACAAC 2892  
  
Qy 419 ACTTTATTTTCTATGTTGTTTTTGCAACATATAGAGTGTGTTTTGAAAAATAAGTACCCATG 478  
|||||  
Db 2893 ACTTTATTTTCTATGTTGTTTTTGCAACATATAGAGTGTGTTTTGAAAAATAAGTACCCATG 2952  
  
Qy 479 TCTTTA 484  
|||||  
Db 2953 TCTTTA 2958



```

; SEQ ID NO 103
; LENGTH: 102
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: m103
; LOCATION: (103)
; OTHER INFORMATION:
US-09-328-475C-1

```

Query Match	88.18;	Score 426.2;	DB 4;	Length 1021;
Best Local Similarity	95.7%;	Pred. No. 2.6e-105;		
Matches 449;	Conservative 0;	Mismatches 18;	Indels 2;	Gaps 1;
Qy	6	AAATAAGCATTTAGTGTCTCAGTCAGTCCTACTGAGTACTCTTTCTCTCCCTCCTCTGAAATTT	65	
Db	561	AATTGCGCCCTTCGAGCGCGCCGCGGCGAGGTACTCTTTCTCTCCCTCCTCTGAAATTT	502	
Qy	66	AATTCTTTCAACTTGCAAATTTGCNAGGATTTACACATTTCACTGATGATGATATATTGCTGTG	125	
Db	501	AATTCTTTCAACTTGCAAATTTGCNAGGATTTACACATTTCACTGATGATGATATATTGCTGTG	442	
Qy	126	CAAAAAAAGAGTGTCTTTGTTTAAAAATTTACTTGGTTTGTGAATCCATCTTCTGCTTTT	185	
Db	441	C-----AAGAGTGTCTTTGTTTAAAAATTTACTTGGTTTGTGAATCCATCTTCTGCTTTT	384	
Qy	186	CCCATTTGGAACCTAGTCAATTAACCCATCTCTGAACTGGTGAAGAAAAATCTGAAGAGCTA	245	
Db	383	CCCATTTGGAACCTAGTCAATTAACCCATCTCTGAACTGGTGAAGAAAAATCTGAAGAGCTA	324	
Qy	246	GTCTATCAGCATCTGACAGGTGAATTCGATGGTTTCTCAGAACCAATTTCAACCACAGACGCC	305	
Db	323	GTCTATCAGCATCTGACAGGTGAATTCGATGGTTTCTCAGAACCAATTTCAACCACAGACGCC	264	
Qy	306	TGTTTCTATCCTGTTTAAATAATAGTGTGGGTTTCTCTACATGCAATAACAAACCCCTGCTC	365	
Db	263	TGTTTCTATCCTGTTTAAATAATAGTGTGGGTTTCTCTACATGCAATAACAAACCCCTGCTC	204	
Qy	366	CAATCTCTCACATAAAGTCTGTGACATTGAAGTTTGTGAGCAGCCGCCACCAACTTTAT	425	
Db	203	CAATCTCTCACATAAAGTCTGTGACATTGAAGTTTGTGAGCAGCCGCCACCAACTTTAT	144	
Qy	426	TTTTTCTATGTTTTTTTTGCAACATATAGTGTTTTTGAAAAATAAGTACC	474	
Db	143	TTTTTCTATGTTTTTTTTGCAACATATAGTGTTTTTGAAAAATAAGTACC	95	

## RESULTS

US-09-328-475C-223/c  
; Sequence 223, Application US/09328475C  
; Patent No. 6476207

## GENERAL INFORMATION:

```

: APPLICANT: Zhang, Jimmy
: APPLICANT: Astel, Jon H.
: APPLICANT: Carroll III, Eddie
: APPLICANT: Endege, Wilson O.
: APPLICANT: Ford, Donna M.
: APPLICANT: Monahan, John E.
: APPLICANT: Schlegel, Robert
: APPLICANT: Steinmann, Kathleen E.
: TITLE OF INVENTION: GENES AND GENE EXPRESSION
: TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED
: FILE REFERENCE: 1532.002/200130.463
: CURRENT APPLICATION NUMBER: US/09/328,475
: CURRENT FILING DATE: 1999-06-09
: NUMBER OF SEQ ID NOS: 341
: SOFTWARE: FastSeq for Windows Version 3.0

```

```

; SEQ ID NO 223
; LENGTH: 822
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: miR-141

```

; LOCATION: (1)...(822)  
 ; OTHER INFORMATION: n = A,T,C or G  
 US-09-328-475C-223

Query Match	85.9%;	Score 415.6;	DB 4;	Length 822;
Best Local Similarity	98.4%;	Pred. No. 1.7e-102;		
Matches 431;	Conservative	0;	Mismatches 4;	Indels 3

Qy	37	GTACTCTTCTCCCTCCCTCGAATTTAATTCCTTTCAACTTGCAGTTCGCAAGGATTA	96
Db	510	GTACTCTTCTCCCTCCCTCGAATTTAATTCCTTTCAACTTGCAGTTCGCAAGGATTA	451
Qy	97	CACATTTCACTGTCGATGTATATGTGTTGCAAAAAAAGAGTCTCTTTGTTAAAAATT	156
Db	450	CACATTTCACTGTCGATGTATATGTGTTGCG--AAAAAAGAGTCTCTTTGTTAAAAATT	394
Qy	157	ACTTGGTTTGTGAATCCATCTTGTTTTTCCCATTTGGAACCTAGTGCATTTAACCCATCTCT	216
Db	393	ACTTGGTTTGTGAATCCATCTTGTTTTTCCCATTTGGAACCTAGTGCATTTAACCCATCTCT	334
Qy	217	GAACCTGGTAGAAAAACATCTCGAAGAGCTAGTCTATCAGCATCTGCAGGTGAATTTGGATG	276
Db	333	GAACCTGGTAGAAAAACATCTCGAAGAGCTAGTCTATCGGCATCTGCAGGTGAATTTGGATG	274
Qy	277	GTTCTCAGAACCATTTCCACCAGACGCTGTTCCTATCTCTGTTTAAATAAATTAGTTTGG	336
Db	273	GTTCTCAGAACCATTTCCACCAGACGCTGTTCCTATCTCTGTTTAAATAAATTAGTTTGG	214
Qy	337	GTTCTCTACATGCATAACAACCCCTGCCTCCAAATCTGTCACATAAAGTCTGTGACTTTGAA	396
Db	213	GTTCTCTACATGCATAACAACCCCTGCCTCCAAATCTGTCACATAAAGTCTGTGACTTTGAA	154
Qy	397	GTTTGTAGTCAGCACCCACCACCAACTTTATTTTCTATGTGTTTGTGTTTGTGCAACATATAGTAGT	456
Db	153	GTTTGTAGTCAGCACCCACCACCAACTTTATTTTCTATGTGTTTGTGTTTGTGCAACATATAGTAGT	94
Qy	457	TTTTGAAATAAAGTACC	474
Db	93	TTTTTGAAATAAAGTACC	76

РЕШЕНИЕ 10

US-09-328-475C-222  
; Sequence 222, Application US/09328475C  
; Patent No. 6476207

## : GENERAL INFORMATION:

1 APPLICANT: Zhang, Jimmy  
 2 APPLICANT: Astel, Jon H.  
 3 APPLICANT: Carroll III, Eddie  
 4 APPLICANT: Endege, Wilson O.  
 5 APPLICANT: Ford, Donna M.  
 6 APPLICANT: Monahan, John E.  
 7 APPLICANT: Schlegel, Robert  
 8 APPLICANT: Steimann, Kathleen E.  
 9 TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT  
 10 TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER  
 11 FILE REFERENCE: 1532.002/200130.463  
 12 CURRENT APPLICATION NUMBER: US/09/328,475C  
 13 CURRENT FILING DATE: 1999-06-09  
 14 NUMBER OF SEQ ID NOS: 341

```
%> BROWSE(US-09-328-475C-222)
%> RECORDS: 1
%> RECORDID: 1
%> RECORDNAME: US-09-328-475C-222
%> RECORDTYPE: DNA
%> ORGANISM: Homo Sapien
%> SEQ ID NO: 222
%> LENGTH: 497
%> TYPE: DNA
```

Query Match	79.1%;	Score 382.8;	DB 4;	Length 497;
Best Local Similarity	98.8%;	Pred. NO. 9e-94;		
Matches 397;	Conservative	0;	Mismatches	2;
			Indels	3

Qy 37 GTACTCTTCTCTCCCTCCCTCTGAATTTAAATCTTCTTCAACTTGCAAATTGCAAGATT 96

Db 99 GTACTCTTCTCCTCCTCTGAAATTAATTTCACTTCACTTGAAGATTA 158  
QY 97 CACATTCAGTGTATATATGTTGCAAAAAAAGTCTCTTTTAAATTT 156  
Db 159 CACATTCAGTGTATATGTTGCAAAAAAAGTCTCTTTTAAATTT 215  
QY 157 ACTTGTGTTGTAATTCATCTGCTTTTCCCATTTGAACCTAGTCTCT 216  
Db 216 ACTTGTGTTGTAATTCATCTGCTTTTCCCATTTGAACCTAGTCTCT 275  
QY 217 GAATCGTGAAGAAACATCTGAAGAGCTAGTCTATCAGCATCTCAGAGGTAATGGATG 276  
Db 276 GAATCGTGAAGAAACATCTGAAGAGCTAGTCTATCAGCATCTCAGAGGTAATGGATG 335  
QY 277 GTTCTCAGAACATTTCCAGAGAGCTGTTTCTATCTCTGTTTAAATAATAGTTGG 336  
Db 336 GTTCTCAGAACATTTCCAGAGAGCTGTTTCTATCTCTGTTTAAATAATAGTTGG 395  
QY 337 GTTCTCAGAACATTTCCAGAGAGCTGTTTCTATCTCTGTTTAAATAATAGTTGG 396  
Db 396 GTTCTCAGAACATTTCCAGAGAGCTGTTTCTATCTCTGTTTAAATAATAGTTGG 455  
QY 397 GTTCTCAGAACATTTCCAGAGAGCTGTTTCTATCTCTGTTTAAATAATAGTTGG 438  
Db 456 GTTCTCAGAACATTTCCAGAGAGCTGTTTCTATCTCTGTTTAAATAATAGTTGG 497

RESULT 11  
US-09-020-956-115  
; Sequence 115, Application US/09020956  
; Patent No. 6261362  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillin, David C.  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO  
; NUMBER OF SEQUENCES: 178  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED AND BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 09-FEB-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.427C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 115:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 366 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:  
; ORGANISM: Homo Sapiens  
US-09-020-956-115

Query Match 75.4%; Score 365; DB 3; Length 366;  
Best Local Similarity 100.0%; Pred. No. 4.9e-89;  
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 CTCTTCTCTCCCTCCTCTGAAATTAATTTCACTTCACTTGAAGATTA 99  
Db 2 CTCTTCTCTCCCTCCTCTGAAATTAATTTCACTTCACTTGAAGATTA 61  
QY 100 ATTCTACTGTGATGTATATGTTGCAAAAAAAGTCTCTTTTAAATTTACT 159  
Db 62 ATTCTACTGTGATGTATATGTTGCAAAAAAAGTCTCTTTTAAATTTACT 121  
QY 160 TGTGTTGTCAATCCATCTTGTCTTTTCCCATTTGAACCTAGTCTATACCCATCTCTGAA 219  
Db 122 TGTGTTGTCAATCCATCTTGTCTTTTCCCATTTGAACCTAGTCTATACCCATCTCTGAA 181  
QY 220 CTGGTAGAAAAACATCTGAAGAGCTAGTCTATCAGCATCTCAGAGGTAATTTGGT 279  
Db 182 CTGGTAGAAAAACATCTGAAGAGCTAGTCTATCAGCATCTCAGAGGTAATTTGGT 241  
QY 280 CTCAGAACCATTTCAACCCAGAGAGCTGTTTCTATCTCTGTTTAAATAATAGTTGGT 339  
Db 242 CTCAGAACCATTTCAACCCAGAGAGCTGTTTCTATCTCTGTTTAAATAATAGTTGGT 301  
QY 340 CTCTACATGCATAACAAACCTGCTCCAAATCTGTACATATAAAGTCTGACTTGAAGTT 399  
Db 302 CTCTACATGCATAACAAACCTGCTCCAAATCTGTACATATAAAGTCTGACTTGAAGTT 361  
QY 400 TAGTC 404  
Db 362 TAGTC 366

RESULT 12  
US-09-030-607-115  
; Sequence 115, Application US/09030607  
; Patent No. 6262245  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillin, David C.  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS  
; NUMBER OF SEQUENCES: 224  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED AND BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 25-FEB-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.427C3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 115:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 366 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:  
; ORGANISM: Homo Sapiens  
US-09-030-607-115

Query Match 75.4%; Score 365; DB 3; Length 366;  
Best Local Similarity 100.0%; Pred. No. 4.9e-89;  
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 CTCTTTCTCTCCCTCCTCTGAAATTAATTTCAACTTTCGAATTTGCAAGGATTACAC 99  
Db 2 CTCTTTCTCTCCCTCCTCTGAAATTAATTTCAACTTTCGAATTTGCAAGGATTACAC 61  
Qy 100 ATTTCACTGTGATGATATATTGTTGCAAAAAAAGTGTCTTTGTTTAAATTAAT 159  
Db 62 ATTTCACTGTGATGATATATTGTTGCAAAAAAAGTGTCTTTGTTTAAATTAAT 121  
Qy 160 TGGTTTGTGAATCAATCTGCTTTTCCCAATTTGGAAGTGTGATTAACCCATCTCGAA 219  
Db 122 TGGTTTGTGAATCAATCTGCTTTTCCCAATTTGGAAGTGTGATTAACCCATCTCGAA 181  
Qy 220 CTGTAGAAAAACATCTGAAAGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGTT 279  
Db 242 CTGTAGAAAAACATCTGAAAGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGTT 241  
Qy 280 CTGAGAACCAATTTTCAACCCAGACAGCCCTGCTCCAATCTGTGCACATAAAAGTCTGTGACTTGAAGTT 339  
Db 242 CTGAGAACCAATTTTCAACCCAGACAGCCCTGCTCCAATCTGTGCACATAAAAGTCTGTGACTTGAAGTT 301  
Qy 340 CTCTACATGATATGATATATTGTTGCAAAAAAAGTGTCTTTGTTTAAATTAAT 399  
Db 122 TGGTTTGTGAATCAATCTGCTTTTCCCAATTTGGAAGTGTGATTAACCCATCTCGAA 181  
Qy 220 CTGTAGAAAAACATCTGAAAGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGTT 279  
Db 182 CTGTAGAAAAACATCTGAAAGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGTT 241  
Qy 280 CTGAGAACCAATTTTCAACCCAGACAGCCCTGCTCCAATCTGTGCACATAAAAGTCTGTGACTTGAAGTT 339  
Db 302 CTCTACATGATATGATATATTGTTGCAAAAAAAGTGTCTTTGTTTAAATTAAT 361  
Qy 400 TAGTC 404  
Db 362 TAGTC 366

RESULT 13  
US-09-439-313-115  
; Sequence 115, Application US/09439313  
; Patent No. 6329505  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jjiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan Louise  
; APPLICANT: Jiang Yuqi  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Kalos, Michael  
; APPLICANT: Fanger, Gary  
; APPLICANT: Retter, Mark  
; APPLICANT: Solk, John  
; APPLICANT: Day, Craig  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
; FILE REFERENCE: 210121.427C9  
; CURRENT APPLICATION NUMBER: US/09/439,313  
; CURRENT FILING DATE: 1999-11-12  
; NUMBER OF SEQ ID NOS: 575  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 115  
; LENGTH: 366  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-439-313-115

Query Match 75.4%; Score 365; DB 4; Length 366;  
Best Local Similarity 100.0%; Pred. No. 4.9e-89;  
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 CTCTTTCTCTCCCTCCTCTGAAATTAATTTCAACTTTCGAATTTGCAAGGATTACAC 99  
Db 2 CTCTTTCTCTCCCTCCTCTGAAATTAATTTCAACTTTCGAATTTGCAAGGATTACAC 61  
Qy 100 ATTTCACTGTGATGATATATTGTTGCAAAAAAAGTGTCTTTGTTTAAATTAAT 159  
Db 62 ATTTCACTGTGATGATATATTGTTGCAAAAAAAGTGTCTTTGTTTAAATTAAT 121

Qy 160 TGGTTTGTGAATCAATCTGCTTTTCCCAATTTGGAAGTGTGATTAACCCATCTCTGAA 219  
Db 122 TGGTTTGTGAATCAATCTGCTTTTCCCAATTTGGAAGTGTGATTAACCCATCTCTGAA 181  
Qy 220 CTGTAGAAAAACATCTGAAAGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGTT 279  
Db 182 CTGTAGAAAAACATCTGAAAGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGTT 241  
Qy 280 CTGAGAACCAATTTTCAACCCAGACAGCCCTGCTCCAATCTGTGCACATAAAAGTCTGTGACTTGAAGTT 339  
Db 242 CTGAGAACCAATTTTCAACCCAGACAGCCCTGCTCCAATCTGTGCACATAAAAGTCTGTGACTTGAAGTT 301  
Qy 340 CTCTACATGATATGATATATTGTTGCAAAAAAAGTGTCTTTGTTTAAATTAAT 399  
Db 302 CTCTACATGATATGATATATTGTTGCAAAAAAAGTGTCTTTGTTTAAATTAAT 361  
Qy 400 TAGTC 404  
Db 362 TAGTC 366

Query Match 75.4%; Score 365; DB 4; Length 366;  
Best Local Similarity 100.0%; Pred. No. 4.9e-89;  
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 CTCTTTCTCTCCCTCCTCTGAAATTAATTTCAACTTTCGAATTTGCAAGGATTACAC 99  
Db 2 CTCTTTCTCTCCCTCCTCTGAAATTAATTTCAACTTTCGAATTTGCAAGGATTACAC 61  
Qy 100 ATTTCACTGTGATGATATATTGTTGCAAAAAAAGTGTCTTTGTTTAAATTAAT 159  
Db 62 ATTTCACTGTGATGATATATTGTTGCAAAAAAAGTGTCTTTGTTTAAATTAAT 121  
Qy 160 TGGTTTGTGAATCAATCTGCTTTTCCCAATTTGGAAGTGTGATTAACCCATCTCTGAA 219  
Db 122 TGGTTTGTGAATCAATCTGCTTTTCCCAATTTGGAAGTGTGATTAACCCATCTCTGAA 181  
Qy 220 CTGTAGAAAAACATCTGAAAGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGTT 279  
Db 182 CTGTAGAAAAACATCTGAAAGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGTT 241  
Qy 280 CTGAGAACCAATTTTCAACCCAGACAGCCCTGCTCCAATCTGTGCACATAAAAGTCTGTGACTTGAAGTT 339  
Db 242 CTGAGAACCAATTTTCAACCCAGACAGCCCTGCTCCAATCTGTGCACATAAAAGTCTGTGACTTGAAGTT 301  
Qy 340 CTCTACATGATATGATATATTGTTGCAAAAAAAGTGTCTTTGTTTAAATTAAT 399  
Db 302 CTCTACATGATATGATATATTGTTGCAAAAAAAGTGTCTTTGTTTAAATTAAT 361

QY 400 TAGTC 404  
Db 362 TAGTC 366

## RESULT 15

US-09-232-149A-115  
: Sequence 115, Application US/09232149A  
: Patent No. 6465611  
: GENERAL INFORMATION:  
: APPLICANT: Xu, Jiangchun  
: APPLICANT: Dillon, Davin C.  
: APPLICANT: Mitcham, Jennifer Lynn  
: TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE  
: FILE REFERENCE: 210121.427C6  
: CURRENT APPLICATION NUMBER: US/09/232,149A  
: NUMBER OF SEQ ID NOS: 338  
: SOFTWARE: FastSeq for Windows Version 3.0  
: SEQ ID NO 115  
: LENGTH: 366  
: TYPE: DNA  
: ORGANISM: Homo sapien  
US-09-232-149A-115

Query Match 75.4%; Score 365; DB 4; Length 366;  
Best Local Similarity 100.0%; Pred. No. 4.9e-89;  
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 40 CTCCTTCTCCCTCCTCTGAAATTAATCTTCAACTTGAATTTGCAAGGATTACAC 99  
Db 2 CTCCTTCTCCCTCCTCTGAAATTAATCTTCAACTTGAATTTGCAAGGATTACAC 61  
QY 100 ATTCACTGTGATGATATATGTTGCAAAAAAAGTCTCTTTTAAAAATTACT 159  
Db 62 ATTCACTGTGATGATATATGTTGCAAAAAAAGTCTCTTTTAAAAATTACT 121  
QY 160 TGGTTTGTGAATCCATCTTGTCTTTTCCCATTTGGAAGTATGTCATTAAACCATCTCTGAA 219  
Db 122 TGGTTTGTGAATCCATCTTGTCTTTTCCCATTTGGAAGTATGTCATTAAACCATCTCTGAA 181  
QY 220 CTGGTAGAAAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAGGTGAATTGGATGTT 279  
Db 182 CTGGTAGAAAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAGGTGAATTGGATGTT 241  
QY 280 CTCAGAACCATTTACCCAGACAGCCTGTTTCTATCCTGTTTAAATAATTAGTTGGTT 339  
Db 242 CTCAGAACCATTTACCCAGACAGCCTGTTTCTATCCTGTTTAAATAATTAGTTGGTT 301  
QY 340 CTCTACATGCATAACAAACCCCTGCTCCAACTGTCTGACATAAAAGTCTGTGACTTGAAGTT 399  
Db 302 CTCTACATGCATAACAAACCCCTGCTCCAACTGTCTGACATAAAAGTCTGTGACTTGAAGTT 361  
QY 400 TAGTC 404  
Db 362 TAGTC 366

Search completed: September 13, 2003, 03:05:40  
Job time : 57 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 13, 2003, 01:57:16 ; Search time 195 Seconds  
(without alignments)  
6025.816 Million cell updates/sec

Title: US-09-352-616A-434

Perfect score: 484

Sequence: 1 tttaaataagcatttagt.....ataaagtaccctgtcttta 484

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1532420 seqs, 1213878141 residues

Total number of hits satisfying chosen parameters: 3264840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 16: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 17: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	484	100.0	484	9	US-09-759-143-434
2	484	100.0	484	9	US-09-780-669-434
3	484	100.0	484	9	US-09-822-827-434
4	484	100.0	484	10	US-09-895-793-434
5	484	100.0	484	9	US-09-895-814-434
6	484	100.0	484	12	US-10-144-678A-434
7	484	100.0	484	13	US-10-012-896-434
8	484	100.0	484	14	US-10-010-940-434
9	473	97.7	755	10	US-09-925-300-258
10	472	97.5	2051	13	US-10-202-193-334
11	472	97.5	2984	9	US-09-759-143-335
12	472	97.5	2984	9	US-09-780-669-335
13	472	97.5	2984	9	US-09-822-827-335
14	472	97.5	2984	10	US-09-232-880-335
15	472	97.5	2984	10	US-09-895-793-335
16	472	97.5	2984	10	US-09-895-814-335

17	472	97.5	2984	12	US-10-144-678A-335	Sequence 335, App	
18	472	97.5	2984	13	US-10-012-896-335	Sequence 335, App	
19	472	97.5	2984	14	US-10-010-940-335	Sequence 335, App	
20	455.4	94.1	3266	14	US-10-205-823-282	Sequence 282, App	
21	426.2	88.1	1020	13	US-10-202-193-102	Sequence 102, App	
22	426.2	88.1	1021	13	US-10-202-193-103	Sequence 103, App	
C	23	415.6	85.9	822	13	US-10-202-193-223	Sequence 223, App
	24	382.8	79.1	497	13	US-10-202-193-222	Sequence 222, App
25	365	75.4	366	9	US-09-759-143-115	Sequence 115, App	
26	365	75.4	366	9	US-09-780-669-115	Sequence 115, App	
27	365	75.4	366	9	US-09-030-606-115	Sequence 115, App	
28	365	75.4	366	9	US-09-822-827-115	Sequence 115, App	
29	365	75.4	366	9	US-09-115-453-115	Sequence 115, App	
30	365	75.4	366	10	US-09-232-880-115	Sequence 115, App	
31	365	75.4	366	10	US-09-895-793-115	Sequence 115, App	
32	365	75.4	366	10	US-09-895-814-115	Sequence 115, App	
33	365	75.4	366	12	US-10-144-678A-115	Sequence 115, App	
34	365	75.4	366	13	US-10-012-896-115	Sequence 115, App	
35	365	75.4	366	14	US-10-010-940-115	Sequence 115, App	
C	36	360	74.4	374	10	US-09-969-708-40	Sequence 40, Appl
	37	332	68.6	335	9	US-09-759-143-141	Sequence 141, App
38	332	68.6	335	9	US-09-780-669-141	Sequence 141, App	
39	332	68.6	335	9	US-09-030-606-141	Sequence 141, App	
40	332	68.6	335	9	US-09-822-827-141	Sequence 141, App	
41	332	68.6	335	9	US-09-115-453-141	Sequence 141, App	
42	332	68.6	335	10	US-09-232-880-141	Sequence 141, App	
43	332	68.6	335	10	US-09-895-793-141	Sequence 141, App	
44	332	68.6	335	10	US-09-895-814-141	Sequence 141, App	
45	332	68.6	335	12	US-10-144-678A-141	Sequence 141, App	

ALIGNMENTS

RESULT 1

US-09-759-143-434  
; Sequence 434, Application US/09759143  
; Patent No. US2002022248A1  
; GENERAL INFORMATION:

- ; APPLICANT: Xu, Jiangchun
- ; APPLICANT: Dillon, Davin C.
- ; APPLICANT: Mitcham, Jennifer L.
- ; APPLICANT: Harlocker, Susan L.
- ; APPLICANT: Jiang, Yuqi
- ; APPLICANT: Henderson, Robert A.
- ; APPLICANT: Kalos, Michael D.
- ; APPLICANT: Fanger, Gary R.
- ; APPLICANT: Retter, Marc W.
- ; APPLICANT: Stolk, John A.
- ; APPLICANT: Day, Craig H.
- ; APPLICANT: Vedvick, Thomas S.
- ; APPLICANT: Carter, Darrick
- ; APPLICANT: Li, Samuel
- ; APPLICANT: Wang, Aijun
- ; APPLICANT: Skeiky, Yasir A.W.
- ; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C23

; CURRENT APPLICATION NUMBER: US/09/759.143

; CURRENT FILING DATE: 2001-01-12

; NUMBER OF SEQ ID NOS: 934

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 434

; LENGTH: 484

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-759-143-434

Query Match 100.0%; Score 484; DB 9; Length 484;  
Best local similarity 100.0%; Pred. No. 7.7e-119;  
Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;









; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Hural, John  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Vinals de Bassols, Carlota  
; APPLICANT: Foy, Teresa  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Watanabe, Yoshihiro  
; APPLICANT: Meagher, Magdelaine Joy  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.427C27  
; CURRENT APPLICATION NUMBER: US/10/012.896  
; CURRENT FILING DATE: 2001-12-10  
; NUMBER OF SEQ ID NOS: 1011  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 434  
; LENGTH: 484  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-012-896-434

Query Match 100.0%; Score 484; DB 13; Length 484;  
Best Local Similarity 100.0%; Pred. No. 7.7e-119;  
Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTTTAAATAGCAATTTAGTGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCCTCTG 60  
Db 1 TTTTAAATAGCAATTTAGTGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCCTCTG 60  
Qy 61 AATTAAATCTTCAACTTGCATTTGCAAGGATTACACATTTTCACGTGATGATATG 120  
Db 61 AATTAAATCTTCAACTTGCATTTGCAAGGATTACACATTTTCACGTGATGATATG 120  
Qy 121 TGTGCAAAAAAAGAGTCTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTTGC 180  
Db 121 TGTGCAAAAAAAGAGTCTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTTGC 180  
Qy 181 TTTTCCCATTTGCACTAGTCTATTAACCATCTCTGAACCTGTTAGTGAATCCATCTGAAG 240  
Db 181 TTTTCCCATTTGCACTAGTCTATTAACCATCTCTGAACCTGTTAGTGAATCCATCTGAAG 240  
Qy 241 AGCTAGTCTATCAGCATCTGACAGTGAATTTGGATGTTCTCAGAACCATTTTACCCAGA 300  
Db 241 AGCTAGTCTATCAGCATCTGACAGTGAATTTGGATGTTCTCAGAACCATTTTACCCAGA 300  
Qy 301 CAGCCTGTTCTATCTCTGTTTAAATAATTTAGTTTGGGTTCTCTACATGCATAAACAACC 360  
Db 301 CAGCCTGTTCTATCTCTGTTTAAATAATTTAGTTTGGGTTCTCTACATGCATAAACAACC 360  
Qy 361 TGCTCCAACTGTCACATAAAAGTCTGTGACTTGAAGTTTGTAGTCAGCACCCCAACAAAC 420  
Db 361 TGCTCCAACTGTCACATAAAAGTCTGTGACTTGAAGTTTGTAGTCAGCACCCCAACAAAC 420  
Qy 421 TTTATTTTCTATCTGTTTGTGCAACATATGAGTGTGTTGAAAATAAAGTACCATGTC 480  
Db 421 TTTATTTTCTATCTGTTTGTGCAACATATGAGTGTGTTGAAAATAAAGTACCATGTC 480  
Qy 481 TTTA 484  
Db 481 TTTA 484

RESULT 8  
US-10-010-940-434  
; Sequence 434, Application US/10010940  
; Publication No. US2003008062A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: P4101  
; CURRENT APPLICATION NUMBER: US/09/925.300

; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan Louise  
; APPLICANT: Jiang Yuqi  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Kalos, Michael  
; APPLICANT: Fanger, Gary  
; APPLICANT: Retter, Mark  
; APPLICANT: Solk, John  
; APPLICANT: Day, Craig  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.427D3  
; CURRENT APPLICATION NUMBER: US/10/010.940  
; CURRENT FILING DATE: 2001-12-05  
; NUMBER OF SEQ ID NOS: 575  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 434  
; LENGTH: 484  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-010-940-434

Query Match 100.0%; Score 484; DB 14; Length 484;  
Best Local Similarity 100.0%; Pred. No. 7.7e-119;  
Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTTTAAATAGCAATTTAGTGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCCTCTG 60  
Db 1 TTTTAAATAGCAATTTAGTGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCCTCTG 60  
Qy 61 AATTAAATCTTCAACTTGCATTTGCAAGGATTACACATTTTCACGTGATGATATG 120  
Db 61 AATTAAATCTTCAACTTGCATTTGCAAGGATTACACATTTTCACGTGATGATATG 120  
Qy 121 TGTGCAAAAAAAGAGTCTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTTGC 180  
Db 121 TGTGCAAAAAAAGAGTCTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTTGC 180  
Qy 181 TTTTCCCATTTGCACTAGTCTATTAACCATCTCTGAACCTGTTAGTGAATCCATCTGAAG 240  
Db 181 TTTTCCCATTTGCACTAGTCTATTAACCATCTCTGAACCTGTTAGTGAATCCATCTGAAG 240  
Qy 241 AGCTAGTCTATCAGCATCTGACAGTGAATTTGGATGTTCTCAGAACCATTTTACCCAGA 300  
Db 241 AGCTAGTCTATCAGCATCTGACAGTGAATTTGGATGTTCTCAGAACCATTTTACCCAGA 300  
Qy 301 CAGCCTGTTCTATCTCTGTTTAAATAATTTAGTTTGGGTTCTCTACATGCATAAACAACC 360  
Db 301 CAGCCTGTTCTATCTCTGTTTAAATAATTTAGTTTGGGTTCTCTACATGCATAAACAACC 360  
Qy 361 TGCTCCAACTGTCACATAAAAGTCTGTGACTTGAAGTTTGTAGTCAGCACCCCAACAAAC 420  
Db 361 TGCTCCAACTGTCACATAAAAGTCTGTGACTTGAAGTTTGTAGTCAGCACCCCAACAAAC 420  
Qy 421 TTTATTTTCTATCTGTTTGTGCAACATATGAGTGTGTTGAAAATAAAGTACCATGTC 480  
Db 421 TTTATTTTCTATCTGTTTGTGCAACATATGAGTGTGTTGAAAATAAAGTACCATGTC 480  
Qy 481 TTTA 484  
Db 481 TTTA 484

RESULT 9  
US-09-925-300-258  
; Sequence 258, Application US/09925300  
; Patent No. US20020151681A1  
; GENERAL INFORMATION:  
; APPLICANT: Craig Ruben,  
; APPLICANT: Steve Ruben  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: P4101  
; CURRENT APPLICATION NUMBER: US/09/925.300

; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05988  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 1890  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 258  
; LENGTH: 755  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (755)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-300-258

Query Match 97.7%; Score 473; DB 10; Length 755;  
Best Local Similarity 99.8%; Pred. No. 8e-116;  
Matches 484; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
QY 1 TTTTAAATAGCAATTTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTG 60
Db 242 TTTTAAATAGCAATTTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTG 301
QY 61 AATTTAAATCTTCAACTTGAATTTGCAAGGATTACAAATTTCACTGTGATATATTG 120
Db 302 AATTTAAATCTTCAACTTGAATTTGCAAGGATTACAAATTTCACTGTGATATATTG 120
QY 121 TGTGTC-AAAAAAGTGTCTTTGTTTAAATTTACTTGTGTTGAATCCATCTTG 179
Db 362 TGTGTC-AAAAAAGTGTCTTTGTTTAAATTTACTTGTGTTGAATCCATCTTG 421
QY 180 CTTTTCCTCCATTTGGAATGATCATTAACCCATCTCTGAACTGGTAGAAAAACATCTGAA 239
Db 422 CTTTTCCTCCATTTGGAATGATCATTAACCCATCTCTGAACTGGTAGAAAAACATCTGAA 481
QY 240 GAGTAGTCTATCAGCATCTGACAGGTGAATTTGATGTTTCTCAGAACCATTTACCCAG 299
Db 482 GAGTAGTCTATCAGCATCTGACAGGTGAATTTGATGTTTCTCAGAACCATTTACCCAG 541
QY 300 ACAGCCGTGTTCTATCTCTGTTTAAATTTAGTTGGGTTCTCTACATGCAATAACACC 359
Db 542 ACAGCCGTGTTCTATCTCTGTTTAAATTTAGTTGGGTTCTCTACATGCAATAACACC 601
QY 360 CTGCTCAATCTGTCACATAAAGTCTGTGACTTTGAAGTTTGTGAGTCTCTACATGCAATAACACC 419
Db 602 CTGCTCAATCTGTCACATAAAGTCTGTGACTTTGAAGTTTGTGAGTCTCTACATGCAATAACACC 661
QY 420 CTTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATAAAGTACCCATGT 479
Db 662 CTTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATAAAGTACCCATGT 721
QY 480 CTTTA 484
Db 722 CTTTA 726
```

RESULT 10  
US-10-202-193-334/c  
; Sequence 334, Application US/10202193  
; Publication NO. US20020192699A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Jimmy  
; APPLICANT: Astel, Jon H.  
; APPLICANT: Carroll III, Eddie  
; APPLICANT: Endege, Wilson O.  
; APPLICANT: Ford, Donna M.  
; APPLICANT: Monahan, John E.  
; APPLICANT: Schlegel, Robert  
; APPLICANT: Stelmann, Kathleen E.  
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT  
; TITLE OF INVENTION: ARE DIFFERENTIALY REGULATED IN PROSTATE CANCER

; FILE REFERENCE: PP-01532.103/200130.463D1  
; CURRENT APPLICATION NUMBER: US/10/202,193  
; CURRENT FILING DATE: 2002-07-23  
; NUMBER OF SEQ ID NOS: 341  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 334  
; LENGTH: 2051  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(2051)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-202-193-334

Query Match 97.5%; Score 472; DB 13; Length 2051;  
Best Local Similarity 99.6%; Pred. No. 2.4e-115;  
Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

```
QY 1 TTTTAAATAGCAATTTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTG 60
Db 854 TTTTAAATAGCAATTTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTG 795
QY 61 AATTTAAATCTTCAACTTGAATTTGCAAGGATTACAAATTTCACTGTGATATATTG 120
Db 794 AATTTAAATCTTCAACTTGAATTTGCAAGGATTACAAATTTCACTGTGATATATTG 735
QY 121 TGTGTC-AAAAAAGTGTCTTTGTTTAAATTTACTTGTGTTGAATCCATCTT 178
Db 734 TGTGTC-AAAAAAGTGTCTTTGTTTAAATTTACTTGTGTTGAATCCATCTT 675
QY 179 GCTTTTCCCATTTGGAATGATCATTAACCCATCTCTGAACTGGTAGAAAAACATCTGA 238
Db 674 GCTTTTCCCATTTGGAATGATCATTAACCCATCTCTGAACTGGTAGAAAAACATCTGA 615
QY 239 AGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGATGTTTCTCAGAACCATTTACCCA 298
Db 614 AGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGATGTTTCTCAGAACCATTTACCCA 555
QY 299 GACAGCTGTTTCTATCTCTGTTTAAATTTAGTTGGGTTCTCTACATGCAATAACACC 358
Db 554 GACAGCTGTTTCTATCTCTGTTTAAATTTAGTTGGGTTCTCTACATGCAATAACACC 495
QY 359 CTGCTCCAATCTGTCACATAAAGTCTGTGACTTTGAAGTTTGTGAGTCTCTACATGCAATAACACC 418
Db 494 CTGCTCCAATCTGTCACATAAAGTCTGTGACTTTGAAGTTTGTGAGTCTCTACATGCAATAACACC 435
QY 419 ACTTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATAAAGTACCCATG 478
Db 434 ACTTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATAAAGTACCCATG 375
QY 479 TCTTTA 484
Db 374 TCTTTA 369
```

RESULT 11  
US-09-759-143-335  
; Sequence 335, Application US/09759143  
; Patent No. US200202248A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqui  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.

```
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 2984
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-335

Query Match      97.5%; Score 472; DB 9; Length 2984;
Best Local Similarity 99.6%; Pred. No. 2.9e-115;
Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 TTTTAAATAAGCATTTAGTGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTCG 60
Db 2473 TTTTAAATAAGCATTTAGTGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTCG 2532
QY 61 AATTTAAATCTTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATGATATATG 120
Db 2533 AATTTAAATCTTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATGATATATG 2592
QY 121 TGTTCG--AAAAAATAAGTGTCTTTGTTTAAATTAATCTTGGTTTGAATCCATCTT 178
Db 2593 TGTTCGAAAAAATAAGTGTCTTTGTTTAAATTAATCTTGGTTTGAATCCATCTT 2652
QY 179 GCTTTTCCCATTTGGAATAGTCAATTAACCATCTCTGAATGGTAGAAAAACATCTGA 238
Db 2653 GCTTTTCCCATTTGGAATAGTCAATTAACCATCTCTGAATGGTAGAAAAACATCTGA 2712
QY 239 AGAGCTAGTCTATCAGCATCTGACAGTGAATGGATGTTCTCGAACCATTTCACCCA 298
Db 2713 AGAGCTAGTCTATCAGCATCTGACAGTGAATGGATGTTCTCGAACCATTTCACCCA 2772
QY 299 GACAGCTGTTTCTATFCCCTTTAATAATTAAGTTGGTTTGGTTCTCTACATGCATAACAAC 358
Db 2773 GACAGCTGTTTCTATFCCCTTTAATAATTAAGTTGGTTTGGTTCTCTACATGCATAACAAC 2832
QY 359 CTTGCTCCAACTGTGCACATAAAAGTCTGTGACTTGAAGTTTAGTCAGCACCCCAAC 418
Db 2833 CTTGCTCCAACTGTGCACATAAAAGTCTGTGACTTGAAGTTTAGTCAGCACCCCAAC 2892
QY 419 ACTTTATTTTCTATGTGTTTTTGCACATATGAGTGTGTTTGAATAAAGTACCACATG 478
Db 2893 ACTTTATTTTCTATGTGTTTTTGCACATATGAGTGTGTTTGAATAAAGTACCACATG 2952
QY 479 TCTTTA 484
Db 2953 TCTTTA 2958
```

## RESULT 12

```
US-09-780-669-335
; Sequence 335, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
```

```
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 2984
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-780-669-335

Query Match      97.5%; Score 472; DB 9; Length 2984;
Best Local Similarity 99.6%; Pred. No. 2.9e-115;
Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 TTTTAAATAAGCATTTAGTGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTCG 60
Db 2473 TTTTAAATAAGCATTTAGTGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTCG 2532
QY 61 AATTTAAATCTTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATGATATATG 120
Db 2533 AATTTAAATCTTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATGATATATG 2592
QY 121 TGTTCG--AAAAAATAAGTGTCTTTGTTTAAATTAATCTTGGTTTGAATCCATCTT 178
Db 2593 TGTTCGAAAAAATAAGTGTCTTTGTTTAAATTAATCTTGGTTTGAATCCATCTT 2652
QY 179 GCTTTTCCCATTTGGAATAGTCAATTAACCATCTCTGAATGGTAGAAAAACATCTGA 238
Db 2653 GCTTTTCCCATTTGGAATAGTCAATTAACCATCTCTGAATGGTAGAAAAACATCTGA 2712
QY 239 AGAGCTAGTCTATCAGCATCTGACAGTGAATGGATGTTCTCGAACCATTTCACCCA 298
Db 2713 AGAGCTAGTCTATCAGCATCTGACAGTGAATGGATGTTCTCGAACCATTTCACCCA 2772
QY 299 GACAGCTGTTTCTATFCCCTTTAATAATTAAGTTGGTTTGGTTCTCTACATGCATAACAAC 358
Db 2773 GACAGCTGTTTCTATFCCCTTTAATAATTAAGTTGGTTTGGTTCTCTACATGCATAACAAC 2832
QY 359 CTTGCTCCAACTGTGCACATAAAAGTCTGTGACTTGAAGTTTAGTCAGCACCCCAAC 418
Db 2833 CTTGCTCCAACTGTGCACATAAAAGTCTGTGACTTGAAGTTTAGTCAGCACCCCAAC 2892
QY 419 ACTTTATTTTCTATGTGTTTTTGCACATATGAGTGTGTTTGAATAAAGTACCACATG 478
Db 2893 ACTTTATTTTCTATGTGTTTTTGCACATATGAGTGTGTTTGAATAAAGTACCACATG 2952
QY 479 TCTTTA 484
Db 2953 TCTTTA 2958
```

## RESULT 13

```
US-09-822-827-335
; Sequence 335, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
```

```

; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 942
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 2984
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-335

```

Query Match 97.5%; Score 472; DB 9; Length 2984;  
Best Local Similarity 99.6%; Pred. No. 2.9e-115;  
Matches 484; Consistency 100.0%;

	1	0	indec1	2	Gaps
QY	1	TTTTAAAAATAGCATTTAGTCTCAGTCCCTACTGAGTACHTCTTCTCCCTCCCTCTG	60		
Db	2473	TTTTAAANATAGCATTTAGTCTCAGTCCCTACTGAGTACTCTTCTCTCCCTCCCTCTG	2532		
QY	61	AATTTAATCTTTCAACTTGCAGGATTACACATTTACAGTGTGATGTATATG	120		
Db	2533	AATTTAATCTTTCAACTTGCAGGATTACACATTTACAGTGTGATGTATATG	2592		
QY	121	TGTTGCG - - AAAAAAAGTGTCTTTGTTTAAAAATTAATCTTGGTTGTGTAATCCATCTT	178		
Db	2593	TGTTGCAAAAAAAGTGTCTTTGTTTAAAAATTAATCTTGGTTGTGTAATCCATCTT	2652		
QY	179	GCTTTTTCCCATTTGGAACTAGTCATTAAGCCCATCTCTGAACHTGGTAGAAAAACATCTGA	238		
Db	2653	GCTTTTTCCCATTTGGAACTAGTCATTAAGCCCATCTCTGAACHTGGTAGAAAAACATCTGA	2712		
QY	239	AGAGCTAGTCTATCAGCATCTGCAGGTCAATTTGGATGTTCTCAGAACCAITTTCAACCA	298		
Db	2713	AGAGCTAGTCTATCAGCATCTGCAGGTCAATTTGGATGTTCTCAGAACCAITTTCAACCA	2772		
QY	299	GACAGCGTGTTCATCTCCTGTTTAATAAATAGTTTGGTTTCTCTACATGCATAACAAC	358		
Db	2773	GACAGCGTGTTCATCTCCTGTTTAATAAATAGTTTGGTTTCTCTACATGCATAACAAC	2832		
QY	359	CCTGCTCCAACTGTGCACATAAAGTCTGTGACTTCAAGTTTAGTCAGACCCCAACAA	418		
Db	2833	CCTGCTCCAACTGTGCACATAAAGTCTGTGACTTCAAGTTTAGTCAGACCCCAACAA	2892		
QY	419	ACTTATATTTTCTATGTGTTTTTTCACACATATAGTGTTTTGAAGTAAAGTACCCATG	478		
Db	2893	ACTTATATTTTCTATGTGTTTTTTCACACATATAGTGTTTTGAAGTAAAGTACCCATG	2952		
QY	479	TCCTTTA 484			
Db	2953	TCCTTTA 2958			

```

RESULT 14
US-09-232-880-335
; Sequence 335, Application US/09232880
; Publication No. US20020182596A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.428C6
; CURRENT APPLICATION NUMBER: US/09/232,880
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 1

```

ORGANISM: Homo sapien  
US-09-232-880-335

; TITLE OF INVENTION: DIAGNOSIS OF PROSTAT  
 ; FILE REFERENCE: 210121.534C2  
 ; CURRENT APPLICATION NUMBER: US/09/895,793  
 ; CURRENT FILING DATE: 2001-06-29

[illegible]

RESULT 15  
US-09-895-793-335  
; Sequence 335, Application US/09895793  
; Publication No. US20020192763A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yiquu  
APPLICANT: Karos, Michael D.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William T.  
APPLICANT: Henderson, Robert A.  
APPLICANT: Hural, John  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Houghton, Raymond L.  
APPLICANT: Vinals de Bassols, Carlota  
APPLICANT: Foy, Teresa

```

/ APPLICANT: Fanger, Gary R.
/
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
/ FILE REFERENCE: 210121.534C2
/ CURRENT APPLICATION NUMBER: US/09/895,793
/ CURRENT FILING DATE: 2001-06-29
/

```

; NUMBER OF SEQ ID NOS: 982  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 335  
; LENGTH: 2984  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-895-793-335

Query Match 97.5%; Score 472; DB 10; Length 2984;

Best Local Similarity 99.6%; Pred. No. 2.9e-115;

Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy	1	TTTTAAATAAGCAATTTAGTGCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCCTCTG	60
Db	2473	TTTTAAATAAGCAATTTAGTGCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCCTCTG	2532
Qy	61	AATTTAATCTTTCAACTTGCAGTTTCAAGGATTACACATTTTCACCTGTGATGATATTTG	120
Db	2533	AATTTAATCTTTCAACTTGCAGTTTCAAGGATTACACATTTTCACCTGTGATGATATTTG	2592
Qy	121	TGTTGC--AAAAAAGTGTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTT	178
Db	2593	TGTTGCAAAAAAAGTGTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTT	2652
Qy	179	GCTTTTCCCATTTGGAAGTGTCTTTAACCCTCTCTGAAGTGGTAGAAAAACATCTGA	238
Db	2653	GCTTTTCCCATTTGGAAGTGTCTTTAACCCTCTCTGAAGTGGTAGAAAAACATCTGA	2712
Qy	239	AGAGTAGTCTATCAGCATCTGACAGGTGAATTTGGATGGTCTCAGAACCATTTTCACCCA	298
Db	2713	AGAGTAGTCTATCAGCATCTGACAGGTGAATTTGGATGGTCTCAGAACCATTTTCACCCA	2772
Qy	299	GACAGCCTGTTTCTATCTCTGTTTAAATTAATTTAGTTTGGGTTCTCTACATGCATAACAAAC	358
Db	2773	GACAGCCTGTTTCTATCTCTGTTTAAATTAATTTAGTTTGGGTTCTCTACATGCATAACAAAC	2832
Qy	359	CCTGCTCAATCTGTACATAAAAGTCTGTGACTTGAAGTTTGTAGTACAGACCCCCACCAA	418
Db	2833	CCTGCTCAATCTGTACATAAAAGTCTGTGACTTGAAGTTTGTAGTACAGACCCCCACCAA	2892
Qy	419	ACTTTATTTTCTATGTGTTTTTTGCAACATATGAGTGTGTTTGAATAAAGTACCCATG	478
Db	2893	ACTTTATTTTCTATGTGTTTTTTGCAACATATGAGTGTGTTTGAATAAAGTACCCATG	2952
Qy	479	TCCTTA 484	
Db	2953	TCCTTA 2958	

Search completed: September 13, 2003, 03:09:03  
Job time : 197 secs

**THIS PAGE BLANK (USPTO)**